

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 3, 2004, 06:21:53 ; Search time 105 Seconds
(without alignments)
78.128 Million cell updates/sec

Title: US-09-733-239-1

Perfect score: 139

Sequence: 1 RILAVERYLKDQQLIGWCSGKLIC 26

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 2672

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 50%

Maximum Match 100%

Listing first 500 summaries

Database :

SPTRMBL 25:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phase:*

10: sp_plant:*

11: sp_podent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriap:*

17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	139	100.0	117	15	Q9YVZ9 human immun
2	139	100.0	117	15	Q9YRU1 human immun
3	139	100.0	122	15	Q9QIU3 human immun
4	139	100.0	122	15	Q9EA97 human immun
5	139	100.0	122	15	Q9WQZ3 human immun
6	139	100.0	122	15	Q9YXP4 human immun
7	139	100.0	122	15	Q7ZJR4 human immun
8	139	100.0	123	15	Q8AEX2 human immun
9	139	100.0	144	15	Q7ZCD7 human immun
10	139	100.0	144	15	Q7ZCD6 human immun
11	139	100.0	145	15	Q7ZC52 human immun
12	139	100.0	145	15	Q7ZC48 human immun
13	139	100.0	155	15	Q8J3N1 human immun
14	139	100.0	357	15	Q7B119 human immun
15	139	100.0	358	15	Q7B120 human immun
16	139	100.0	588	15	Q993A8 human immun

17	139	100.0	588	15	Q993A7	Q993A7 human immun
18	139	100.0	589	15	Q993B1	Q993B1 human immun
19	139	100.0	590	15	Q993A9	Q993A9 human immun
20	139	100.0	616	15	Q993B0	Q993B0 human immun
21	139	100.0	618	15	Q993B2	Q993B2 human immun
22	139	100.0	727	15	Q9Q723	Q9Q723 human immun
23	139	100.0	747	15	Q70607	Q70607 human immun
24	139	100.0	748	15	Q70606	Q70606 human immun
25	139	100.0	752	15	Q70604	Q70604 human immun
26	139	100.0	752	15	Q70605	Q70605 human immun
27	139	100.0	752	15	Q70608	Q70608 human immun
28	139	100.0	757	15	Q9Q722	Q9Q722 human immun
29	139	100.0	800	15	Q9MMV1	Q9MMV1 human immun
30	139	100.0	801	15	Q9MMU9	Q9MMU9 human immun
31	139	100.0	807	15	Q8Q2X2	Q8Q2X2 human immun
32	139	100.0	809	15	Q9MMV0	Q9MMV0 human immun
33	139	100.0	826	15	Q9DVL1	Q9DVL1 human immun
34	139	100.0	845	15	Q9ID89	Q9ID89 human immun
35	139	100.0	847	15	Q69996	Q69996 human immun
36	139	100.0	849	15	Q9YKT7	Q9YKT7 human immun
37	139	100.0	849	15	Q9OC19	Q9OC19 human immun
38	139	100.0	849	15	Q9YKT4	Q9YKT4 human immun
39	139	100.0	850	15	Q9QBY2	Q9QBY2 human immun
40	139	100.0	851	15	Q9QBZ4	Q9QBZ4 human immun
41	139	100.0	854	15	Q56566	Q56566 human immun
42	139	100.0	854	15	Q85582	Q85582 human immun
43	139	100.0	854	15	Q8UNL0	Q8UNL0 human immun
44	139	100.0	854	15	Q72502	Q72502 human immun
45	139	100.0	854	15	Q90178	Q90178 human immun
46	139	100.0	854	15	Q9DVL2	Q9DVL2 human immun
47	139	100.0	854	15	Q78705	Q78705 human immun
48	139	100.0	855	15	Q8AQV7	Q8AQV7 human immun
49	139	100.0	856	15	Q74090	Q74090 human immun
50	139	100.0	856	15	Q92877	Q92877 simian-huma
51	139	100.0	856	15	Q74599	Q74599 human immun
52	139	100.0	857	15	Q92822	Q92822 human immun
53	139	100.0	857	15	Q71013	Q71013 human immun
54	139	100.0	857	15	Q89654	Q89654 human immun
55	139	100.0	857	15	Q92823	Q92823 human immun
56	139	100.0	857	15	Q9QB20	Q9QB20 human immun
57	139	100.0	859	15	Q9YUZ4	Q9YUZ4 human immun
58	139	100.0	859	15	Q9WLJ1	Q9WLJ1 human immun
59	139	100.0	860	15	Q7SQA7	Q7SQA7 human immun
60	139	100.0	862	15	Q8UNL9	Q8UNL9 human immun
61	139	100.0	862	15	Q7SQA2	Q7SQA2 human immun
62	139	100.0	864	15	Q9YBP3	Q9YBP3 human immun
63	139	100.0	864	15	Q7ZJC8	Q7ZJC8 human immun
64	139	100.0	866	15	Q9WPZ4	Q9WPZ4 human immun
65	139	100.0	868	15	Q8ADN9	Q8ADN9 human immun
66	139	100.0	870	15	Q8Q2X1	Q8Q2X1 human immun
67	139	100.0	870	15	Q8Q2X0	Q8Q2X0 human immun
68	138	99.3	94	15	Q8AEX3	Q8AEX3 human immun
69	138	99.3	109	15	Q40239	Q40239 human immun
70	138	99.3	112	15	Q8UQW2	Q8UQW2 human immun
71	138	99.3	117	15	Q9QKN5	Q9QKN5 human immun
72	138	99.3	117	15	Q9YRT2	Q9YRT2 human immun
73	138	99.3	117	15	Q9YRS4	Q9YRS4 human immun
74	138	99.3	117	15	Q9QKN0	Q9QKN0 human immun
75	138	99.3	117	15	Q9YZ04	Q9YZ04 human immun
76	138	99.3	117	15	Q9YRS6	Q9YRS6 human immun
77	138	99.3	117	15	Q9WKU0	Q9WKU0 human immun
78	138	99.3	117	15	Q9WM72	Q9WM72 human immun
79	138	99.3	117	15	Q9QKN3	Q9QKN3 human immun
80	138	99.3	117	15	Q9YZ01	Q9YZ01 human immun
81	138	99.3	117	15	Q9YRS2	Q9YRS2 human immun
82	138	99.3	117	15	Q9YRZ2	Q9YRZ2 human immun
83	138	99.3	117	15	Q7SVI8	Q7SVI8 human immun
84	138	99.3	117	15	Q7SVI4	Q7SVI4 human immun
85	138	99.3	117	15	Q7SVG4	Q7SVG4 human immun
86	138	99.3	117	15	Q7SVG1	Q7SVG1 human immun
87	138	99.3	117	15	Q7SVF9	Q7SVF9 human immun
88	138	99.3	117	15	Q7SVF7	Q7SVF7 human immun
89	138	99.3	117	15	Q7SVF4	Q7SVF4 human immun

90	138	99.3	117	15	Q7SVF3	Q7svf3 human	163	138	99.3	122	15	Q9IUN6	Q9ijn6 human
91	138	99.3	117	15	Q7SVF2	Q7svf2 human	164	138	99.3	122	15	Q9ODR2	Q9odr2 human
92	138	99.3	117	15	Q7SVF8	Q7svf8 human	165	138	99.3	122	15	Q9ODP8	Q9odp8 human
93	138	99.3	117	15	Q7SVF7	Q7svf7 human	166	138	99.3	122	15	Q9ILJ6	Q9ilj6 human
94	138	99.3	117	15	Q7SVF4	Q7svf4 human	167	138	99.3	122	15	Q9IJP6	Q9ijp6 human
95	138	99.3	118	15	Q9ESK0	Q9esr0 human	168	138	99.3	122	15	Q9EA88	Q9ea88 human
96	138	99.3	121	15	Q9ODU5	Q9odj5 human	169	138	99.3	122	15	Q9ODS1	Q9ods1 human
97	138	99.3	121	15	Q9EA94	Q9ea94 human	170	138	99.3	122	15	Q9IJQ6	Q9ijq6 human
98	138	99.3	122	15	Q9ODJ2	Q9odj2 human	171	138	99.3	122	15	Q9IQJ5	Q9iqj5 human
99	138	99.3	122	15	Q9IJN0	Q9ijn0 human	172	138	99.3	122	15	Q9ODK2	Q9odk2 human
100	138	99.3	122	15	Q9EA85	Q9ea85 human	173	138	99.3	122	15	Q9ODN1	Q9odn1 human
101	138	99.3	122	15	Q9QIW8	Q9qiw8 human	174	138	99.3	122	15	Q9ODM2	Q9odm2 human
102	138	99.3	122	15	Q9QIW1	Q9qiw1 human	175	138	99.3	122	15	Q9ODN3	Q9odn3 human
103	138	99.3	122	15	Q9EA81	Q9ea81 human	176	138	99.3	122	15	Q9IJP2	Q9ijp2 human
104	138	99.3	122	15	Q9YX00	Q9yxq0 human	177	138	99.3	122	15	Q9ODS7	Q9ods7 human
105	138	99.3	122	15	Q9EA84	Q9ea84 human	178	138	99.3	122	15	Q9QIU7	Q9qiu7 human
106	138	99.3	122	15	Q9QIW0	Q9qiw0 human	179	138	99.3	122	15	Q9IJQ1	Q9ijq1 human
107	138	99.3	122	15	Q9ODQ9	Q9odq9 human	180	138	99.3	122	15	Q9WR01	Q9wr01 human
108	138	99.3	122	15	Q9IJN1	Q9ijn1 human	181	138	99.3	122	15	Q9IJL1	Q9ijl1 human
109	138	99.3	122	15	Q9ODK8	Q9odk8 human	182	138	99.3	122	15	Q9IJM9	Q9ijm9 human
110	138	99.3	122	15	Q9ODS5	Q9ods5 human	183	138	99.3	122	15	Q9IJQ9	Q9ijq9 human
111	138	99.3	122	15	Q9ODQ4	Q9odq4 human	184	138	99.3	122	15	Q9IQJ5	Q9iqj5 human
112	138	99.3	122	15	Q9EA85	Q9ea85 human	185	138	99.3	122	15	Q9ILM2	Q9ilm2 human
113	138	99.3	122	15	Q9IJM8	Q9ijm8 human	186	138	99.3	122	15	Q9ODT2	Q9odt2 human
114	138	99.3	122	15	Q9EA82	Q9ea82 human	187	138	99.3	122	15	Q9YXP3	Q9yxp3 human
115	138	99.3	122	15	Q9ODL1	Q9odl1 human	188	138	99.3	122	15	Q9EA82	Q9ea82 human
116	138	99.3	122	15	Q9ODS4	Q9ods4 human	189	138	99.3	122	15	Q9ODK7	Q9odk7 human
117	138	99.3	122	15	Q9QIW3	Q9qiw3 human	190	138	99.3	122	15	Q9IJQ4	Q9ijq4 human
118	138	99.3	122	15	Q9OPX7	Q9opx7 human	191	138	99.3	122	15	Q9ODM3	Q9odm3 human
119	138	99.3	122	15	Q9QIV8	Q9qiv8 human	192	138	99.3	122	15	Q9ODL6	Q9odl6 human
120	138	99.3	122	15	Q9WQZ1	Q9wqz1 human	193	138	99.3	122	15	Q9WQZ4	Q9wqz4 human
121	138	99.3	122	15	Q9OPV1	Q9opv1 human	194	138	99.3	122	15	Q9YXN5	Q9yxn5 human
122	138	99.3	122	15	Q9ILL3	Q9ill3 human	195	138	99.3	122	15	Q9QIU8	Q9qiu8 human
123	138	99.3	122	15	Q9ODN6	Q9odn6 human	196	138	99.3	122	15	Q9QIU8	Q9qiu8 human
124	138	99.3	122	15	Q9QIV7	Q9qiv7 human	197	138	99.3	122	15	Q9ODN5	Q9odn5 human
125	138	99.3	122	15	Q9ODP5	Q9odp5 human	198	138	99.3	122	15	Q9IJP7	Q9ijp7 human
126	138	99.3	122	15	Q9ODT0	Q9odt0 human	199	138	99.3	122	15	Q9ODL2	Q9odl2 human
127	138	99.3	122	15	Q9IJK5	Q9ijk5 human	200	138	99.3	122	15	Q7ZJS6	Q7zjs6 human
128	138	99.3	122	15	Q9YXN7	Q9yxn7 human	201	138	99.3	122	15	Q7ZJS2	Q7zjs2 human
129	138	99.3	122	15	Q9ODP0	Q9odp0 human	202	138	99.3	122	15	Q7ZJS1	Q7zjs1 human
130	138	99.3	122	15	Q9WQZ7	Q9wqz7 human	203	138	99.3	122	15	Q7ZJS0	Q7zjs0 human
131	138	99.3	122	15	Q9ODQ7	Q9odq7 human	204	138	99.3	122	15	Q7ZJR8	Q7zjr8 human
132	138	99.3	122	15	Q9ILK4	Q9ilk4 human	205	138	99.3	122	15	Q7ZJR7	Q7zjr7 human
133	138	99.3	122	15	Q9YXN4	Q9yxn4 human	206	138	99.3	122	15	Q7ZJR6	Q7zjr6 human
134	138	99.3	122	15	Q9QIW7	Q9qiw7 human	207	138	99.3	122	15	Q7ZJR5	Q7zjr5 human
135	138	99.3	122	15	Q9EA84	Q9ea84 human	208	138	99.3	122	15	Q7ZJP0	Q7zjp0 human
136	138	99.3	122	15	Q9IJQ8	Q9ijq8 human	209	138	99.3	123	15	Q8J3S3	Q8j3s3 human
137	138	99.3	122	15	Q9YXR0	Q9yxr0 human	210	138	99.3	123	15	Q8J3R5	Q8j3r5 human
138	138	99.3	122	15	Q9ODN0	Q9odn0 human	211	138	99.3	123	15	Q9YXR3	Q9yxr3 human
139	138	99.3	122	15	Q9YXQ7	Q9yxq7 human	212	138	99.3	123	15	Q8J3S2	Q8j3s2 human
140	138	99.3	122	15	Q9YXP9	Q9yxp9 human	213	138	99.3	123	15	Q8AEX1	Q8aex1 human
141	138	99.3	122	15	Q9ODI9	Q9odi9 human	214	138	99.3	124	15	Q8J3R7	Q8j3r7 human
142	138	99.3	122	15	Q9ODN2	Q9odn2 human	215	138	99.3	124	15	Q9YZ03	Q9yz03 human
143	138	99.3	122	15	Q9YXR4	Q9yxr4 human	216	138	99.3	125	15	Q9IWP9	Q9iwp9 human
144	138	99.3	122	15	Q9IJQ7	Q9ijq7 human	217	138	99.3	126	15	Q9IWP9	Q9iwp9 human
145	138	99.3	122	15	Q9IJL2	Q9ijl2 human	218	138	99.3	127	15	Q9YXK6	Q9yxk6 human
146	138	99.3	122	15	Q9ODR7	Q9odr7 human	219	138	99.3	127	15	Q9IWR0	Q9iwr0 human
147	138	99.3	122	15	Q9ODR8	Q9odr8 human	220	138	99.3	127	15	Q9WM82	Q9wm82 human
148	138	99.3	122	15	Q9YXQ1	Q9yxq1 human	221	138	99.3	127	15	Q9WM85	Q9wm85 human
149	138	99.3	122	15	Q9ODN9	Q9odn9 human	222	138	99.3	127	15	Q9IYW8	Q9iyw8 human
150	138	99.3	122	15	Q9QIV3	Q9qiv3 human	223	138	99.3	128	15	Q9IHY1	Q9ihy1 human
151	138	99.3	122	15	Q9IJL3	Q9ijl3 human	224	138	99.3	129	15	Q9YVZ0	Q9yvz0 human
152	138	99.3	122	15	Q9EA95	Q9ea95 human	225	138	99.3	129	15	Q9YVY2	Q9yvy2 human
153	138	99.3	122	15	Q9ODL7	Q9odl7 human	226	138	99.3	129	15	Q9IWR6	Q9iwr6 human
154	138	99.3	122	15	Q9ODQ8	Q9odq8 human	227	138	99.3	130	15	Q9IYW6	Q9iyw6 human
155	138	99.3	122	15	Q9ODJ1	Q9odj1 human	228	138	99.3	132	15	Q9IWO0	Q9iwo0 human
156	138	99.3	122	15	Q9YXN8	Q9yxm8 human	229	138	99.3	133	15	Q8UQZ6	Q8uqz6 human
157	138	99.3	122	15	Q9ODI8	Q9odi8 human	230	138	99.3	133	15	Q8UQW8	Q8uqw8 human
158	138	99.3	122	15	Q9IJN7	Q9ijn7 human	231	138	99.3	133	15	Q9YZ13	Q9yz13 human
159	138	99.3	122	15	Q9QDS6	Q9qds6 human	232	138	99.3	133	15	Q9Q018	Q9q018 human
160	138	99.3	122	15	Q9ODP3	Q9odp3 human	233	138	99.3	133	15	Q9Q057	Q9q057 human
161	138	99.3	122	15	Q9ODK0	Q9odk0 human	234	138	99.3	133	15	Q9Q063	Q9q063 human
162	138	99.3	122	15	Q9ODR3	Q9odr3 human	235	138	99.3	133	15	Q90PZ3	Q90pz3 human

236	138	99.3	133	15	Q90Q37	Q90q37	human	immun	309	138	99.3	201	15	Q8JAL8	Q8jal8	human	immun
237	138	99.3	133	15	Q8UQ24	Q8uq24	human	immun	310	138	99.3	217	15	Q8JAM0	Q8jam0	human	immun
238	138	99.3	133	15	Q90Q25	Q90q25	human	immun	311	138	99.3	225	15	Q90IC1	Q90ic1	human	immun
239	138	99.3	133	15	Q8UQ23	Q8uq23	human	immun	312	138	99.3	225	15	Q99IB9	Q99ib9	human	immun
240	138	99.3	133	15	Q91WR3	Q91wr3	human	immun	313	138	99.3	225	15	Q99IC4	Q99ic4	human	immun
241	138	99.3	133	15	Q90Q27	Q90q27	human	immun	314	138	99.3	225	15	Q99IC3	Q99ic3	human	immun
242	138	99.3	133	15	Q90Q35	Q90q35	human	immun	315	138	99.3	225	15	Q99IC5	Q99ic5	human	immun
243	138	99.3	134	15	Q91WQ6	Q91wq6	human	immun	316	138	99.3	225	15	Q99IC0	Q99ic0	human	immun
244	138	99.3	136	15	Q8UQ25	Q8uq25	human	immun	317	138	99.3	357	15	Q78118	Q78118	human	immun
245	138	99.3	137	15	Q9DPQMO	Q9dpm0	human	immun	318	138	99.3	357	15	Q78156	Q78156	human	immun
246	138	99.3	139	15	Q7SLZ5	Q7slz5	human	immun	319	138	99.3	357	15	Q78112	Q78112	human	immun
247	138	99.3	140	15	Q7SM28	Q7sm28	human	immun	320	138	99.3	357	15	Q78155	Q78155	human	immun
248	138	99.3	143	15	Q91WQ1	Q91wq1	human	immun	321	138	99.3	362	15	Q9WIT0	Q9wit0	human	immun
249	138	99.3	144	15	Q91WP3	Q91wp3	human	immun	322	138	99.3	380	15	Q8QDX2	Q8qdx2	human	immun
250	138	99.3	144	15	Q70207	Q70207	human	immun	323	138	99.3	387	15	Q8QEI1	Q8qe11	human	immun
251	138	99.3	144	15	Q70206	Q70206	human	immun	324	138	99.3	387	15	Q8QEI5	Q8qe15	human	immun
252	138	99.3	144	15	Q7ZCE9	Q7zce9	human	immun	325	138	99.3	387	15	Q8QEO7	Q8qe07	human	immun
253	138	99.3	144	15	Q7ZCE2	Q7zce2	human	immun	326	138	99.3	392	15	Q8J511	Q8j511	human	immun
254	138	99.3	144	15	Q7ZCE1	Q7zce1	human	immun	327	138	99.3	398	15	Q72603	Q72603	human	immun
255	138	99.3	144	15	Q7ZCE0	Q7zce0	human	immun	328	138	99.3	416	15	Q72602	Q72602	human	immun
256	138	99.3	144	15	Q7ZCDB8	Q7zcd8	human	immun	329	138	99.3	416	15	Q8J513	Q8j513	human	immun
257	138	99.3	144	15	Q7ZCC6	Q7zcc6	human	immun	330	138	99.3	421	15	Q8J514	Q8j514	human	immun
258	138	99.3	144	15	Q7ZCC5	Q7zcc5	human	immun	331	138	99.3	546	15	Q41643	Q41643	human	immun
259	138	99.3	144	15	Q7ZCC2	Q7zcc2	human	immun	332	138	99.3	605	15	Q73363	Q73363	human	immun
260	138	99.3	144	15	Q7ZCB9	Q7zcb9	human	immun	333	138	99.3	606	15	Q9Q6V8	Q9q6v8	human	immun
261	138	99.3	144	15	Q7ZCB8	Q7zcb8	human	immun	334	138	99.3	616	15	Q8Q859	Q8q859	human	immun
262	138	99.3	144	15	Q7ZCB5	Q7zcb5	human	immun	335	138	99.3	679	15	Q9IK02	Q9ik02	human	immun
263	138	99.3	144	15	Q7ZCB4	Q7zcb4	human	immun	336	138	99.3	684	15	Q9IK06	Q9ik06	human	immun
264	138	99.3	144	15	Q7ZCB1	Q7zcb1	human	immun	337	138	99.3	729	15	Q8Q856	Q8q856	human	immun
265	138	99.3	144	15	Q7ZCB0	Q7zcb0	human	immun	338	138	99.3	797	15	Q9IW14	Q9iw14	human	immun
266	138	99.3	144	15	Q7ZCA6	Q7zca6	human	immun	339	138	99.3	797	15	Q03808	Q03808	human	immun
267	138	99.3	144	15	Q7ZCA5	Q7zca5	human	immun	340	138	99.3	797	15	Q03810	Q03810	human	immun
268	138	99.3	144	15	Q7ZC98	Q7zc98	human	immun	341	138	99.3	799	15	Q03807	Q03807	human	immun
269	138	99.3	144	15	Q7ZC96	Q7zc96	human	immun	342	138	99.3	801	15	Q03809	Q03809	human	immun
270	138	99.3	144	15	Q7ZC95	Q7zc95	human	immun	343	138	99.3	802	15	Q9QP04	Q9qp04	human	immun
271	138	99.3	144	15	Q7ZC71	Q7zc71	human	immun	344	138	99.3	807	15	Q76121	Q76121	human	immun
272	138	99.3	144	15	Q7ZC70	Q7zc70	human	immun	345	138	99.3	813	15	Q41530	Q41530	human	immun
273	138	99.3	145	15	Q7ZC66	Q7zc66	human	immun	346	138	99.3	832	15	Q9QSQ7	Q9qsq7	human	immun
274	138	99.3	145	15	Q7ZC49	Q7zc49	human	immun	347	138	99.3	835	15	Q76074	Q76074	human	immun
275	138	99.3	145	15	Q7ZC39	Q7zc39	human	immun	348	138	99.3	837	15	Q8JDN0	Q8jdn0	human	immun
276	138	99.3	145	15	Q7ZC33	Q7zc33	human	immun	349	138	99.3	837	15	Q8JDM6	Q8jdm6	human	immun
277	138	99.3	145	15	Q7ZC32	Q7zc32	human	immun	350	138	99.3	838	15	Q9Q6V0	Q9q6v0	human	immun
278	138	99.3	146	15	Q7ZC68	Q7zc68	human	immun	351	138	99.3	839	15	Q73364	Q73364	human	immun
279	138	99.3	146	15	Q7ZC30	Q7zc30	human	immun	352	138	99.3	840	15	Q9QNX7	Q9qnx7	human	immun
280	138	99.3	146	15	Q7SM37	Q7sm37	human	immun	353	138	99.3	840	15	Q8QDW5	Q8qdw5	human	immun
281	138	99.3	147	15	Q7SM44	Q7sm44	human	immun	354	138	99.3	840	15	Q9QSU2	Q9qsu2	human	immun
282	138	99.3	155	15	Q8J3N3	Q8j3n3	human	immun	355	138	99.3	841	15	Q9DVL7	Q9dvl7	human	immun
283	138	99.3	155	15	Q8J3Q1	Q8j3q1	human	immun	356	138	99.3	842	15	Q9DVK7	Q9dvk7	human	immun
284	138	99.3	156	15	Q8JAL7	Q8jal7	human	immun	357	138	99.3	842	15	Q7ZMG7	Q7zmg7	human	immun
285	138	99.3	156	15	Q8J3Q9	Q8j3q9	human	immun	358	138	99.3	842	15	Q8JDL4	Q8jdl4	human	immun
286	138	99.3	163	15	Q9QEB0	Q9qe80	human	immun	359	138	99.3	843	15	Q9QKI8	Q9qki8	human	immun
287	138	99.3	163	15	Q9QE76	Q9qe76	human	immun	360	138	99.3	843	15	Q70150	Q70150	human	immun
288	138	99.3	163	15	Q9QEB9	Q9qe69	human	immun	361	138	99.3	843	15	Q9QKH8	Q9qkh8	human	immun
289	138	99.3	163	15	Q9QEB73	Q9qe73	human	immun	362	138	99.3	843	15	Q70008	Q70008	human	immun
290	138	99.3	163	15	Q9QEB67	Q9qe67	human	immun	363	138	99.3	843	15	Q9QKI6	Q9qki6	human	immun
291	138	99.3	163	15	Q9QEB68	Q9qe68	human	immun	364	138	99.3	844	15	Q73298	Q73298	human	immun
292	138	99.3	163	15	Q9QEB71	Q9qe71	human	immun	365	138	99.3	844	15	Q70138	Q70138	human	immun
293	138	99.3	163	15	Q9QEB74	Q9qe74	human	immun	366	138	99.3	844	15	Q9IMJ2	Q9imj2	human	immun
294	138	99.3	163	15	Q9QEB72	Q9qe72	human	immun	367	138	99.3	845	15	Q8UMH0	Q8umh0	human	immun
295	138	99.3	163	15	Q9QEB65	Q9qe65	human	immun	368	138	99.3	845	15	Q9WB73	Q9wbt3	human	immun
296	138	99.3	164	15	Q8J3R2	Q8j3r2	human	immun	369	138	99.3	845	15	Q70679	Q70679	human	immun
297	138	99.3	164	15	Q9QEB78	Q9qe78	human	immun	370	138	99.3	845	15	Q41797	Q41797	human	immun
298	138	99.3	164	15	Q9QEB81	Q9qe81	human	immun	371	138	99.3	845	15	Q7SV04	Q7sv04	human	immun
299	138	99.3	164	15	Q9QEB64	Q9qe64	human	immun	372	138	99.3	846	15	Q8Q855	Q8q855	human	immun
300	138	99.3	164	15	Q9QEB70	Q9qe70	human	immun	373	138	99.3	846	15	Q56111	Q56111	human	immun
301	138	99.3	164	15	Q9QEB82	Q9qe82	human	immun	374	138	99.3	846	15	Q8USW0	Q8usw0	human	immun
302	138	99.3	180	15	Q8JER3	Q8jer3	human	immun	375	138	99.3	847	15	Q8Q854	Q8q854	human	immun
303	138	99.3	181	15	Q8JER4	Q8jer4	human	immun	376	138	99.3	847	15	P88525	P88525	human	immun
304	138	99.3	180	15	Q8JAK8	Q8jak8	human	immun	377	138	99.3	847	15	Q9WIS1	Q9wis1	human	immun
305	138	99.3	190	15	Q8JAJ7	Q8jaj7	human	immun	378	138	99.3	847	15	Q90MM3	Q90mm3	human	immun
306	138	99.3	192	15	Q8JAL2	Q8jal2	human	immun	379	138	99.3	847	15	Q8AR21	Q8ar21	human	immun
307	138	99.3	199	15	Q8JAL3	Q8jal3	human	immun	380	138	99.3	847	15	Q7ZMH5	Q7zmh5	human	immun
308	138	99.3	201	15	Q8JAL5	Q8jal5	human	immun	381	138	99.3	847	15	Q7ZB26	Q7zb26	human	immun

382	138	99.3	847	15	Q7ZB25	Q7zbz5 human immun
383	138	99.3	848	15	Q9IV28	Q9iv28 human immun
384	138	99.3	848	15	Q9WC60	Q9wc60 human immun
385	138	99.3	848	15	Q7ZB21	Q7zb21 human immun
386	138	99.3	849	15	O11944	O11944 human immun
387	138	99.3	849	15	Q9IEN3	Q9ibn3 human immun
388	138	99.3	849	15	Q8Q851	Q8q851 human immun
389	138	99.3	849	15	Q8J9B8	Q8j9b8 human immun
390	138	99.3	849	15	Q7ZJG6	Q7zjg6 human immun
391	138	99.3	849	15	Q8JDH9	Q8jd9 human immun
392	138	99.3	850	15	O41591	O41591 human immun
393	138	99.3	850	15	Q9WC69	Q9wc69 human immun
394	138	99.3	850	15	Q70003	Q70003 human immun
395	138	99.3	850	15	O11946	O11946 human immun
396	138	99.3	850	15	Q7SVL4	Q7svl4 human immun
397	138	99.3	851	15	O41641	O41641 human immun
398	138	99.3	851	15	O56110	O56110 human immun
399	138	99.3	851	15	Q8Q852	Q8q852 human immun
400	138	99.3	851	15	Q9QBY6	Q9qby6 human immun
401	138	99.3	851	15	Q8Q853	Q8q853 human immun
402	138	99.3	851	15	O56562	O56562 human immun
403	138	99.3	851	15	Q9Q6U7	Q9q6u7 human immun
404	138	99.3	851	15	Q7ZML4	Q7zml4 human immun
405	138	99.3	852	15	O41580	O41580 human immun
406	138	99.3	852	15	Q8UPQ5	Q8upq5 human immun
407	138	99.3	852	15	Q8UL54	Q8ul54 human immun
408	138	99.3	852	15	Q9Q705	Q9q705 human immun
409	138	99.3	852	15	O73303	O73303 human immun
410	138	99.3	852	15	O56567	O56567 human immun
411	138	99.3	852	15	Q7ZB27	Q7zb27 human immun
412	138	99.3	853	15	Q8JD13	Q8jd13 human immun
413	138	99.3	853	15	Q9J022	Q9j022 human immun
414	138	99.3	853	15	Q9YMY8	Q9ymy8 human immun
415	138	99.3	853	15	O56108	O56108 human immun
416	138	99.3	853	15	Q9J023	Q9j023 human immun
417	138	99.3	853	15	Q9WS45	Q9ws45 human immun
418	138	99.3	853	15	Q9WB15	Q9wb15 human immun
419	138	99.3	853	15	Q8AF21	Q8af21 human immun
420	138	99.3	853	15	Q7ZJF5	Q7zjf5 human immun
421	138	99.3	853	15	Q8JDL1	Q8jdl1 human immun
422	138	99.3	853	15	Q7SVL6	Q7svl6 human immun
423	138	99.3	853	15	Q7SUR3	Q7sur3 human immun
424	138	99.3	853	15	Q7SUR2	Q7sur2 human immun
425	138	99.3	853	15	Q7SIK0	Q7sik0 human immun
426	138	99.3	854	15	Q92875	Q92875 human immun
427	138	99.3	854	15	Q8USY7	Q8usy7 human immun
428	138	99.3	854	15	Q73300	Q73300 human immun
429	138	99.3	854	15	Q9YV14	Q9yv14 human immun
430	138	99.3	854	15	O92762	O92762 human immun
431	138	99.3	854	15	O56112	O56112 human immun
432	138	99.3	854	15	Q9IJZ9	Q9ijz9 human immun
433	138	99.3	854	15	Q9Q720	Q9q720 human immun
434	138	99.3	854	15	O8ACA7	O8aca7 human immun
435	138	99.3	854	15	Q7SVL3	Q7svl3 human immun
436	138	99.3	855	15	Q9WB14	Q9wb14 human immun
437	138	99.3	855	15	Q9EL87	Q9el87 human immun
438	138	99.3	855	15	Q90266	Q90266 human immun
439	138	99.3	855	15	Q7SVL0	Q7svl0 human immun
440	138	99.3	855	15	Q7SUS7	Q7sus7 human immun
441	138	99.3	855	15	Q7SUS6	Q7sus6 human immun
442	138	99.3	855	15	Q7SUS5	Q7sus5 human immun
443	138	99.3	855	15	Q7SUS4	Q7sus4 human immun
444	138	99.3	855	15	Q7SUS2	Q7sus2 human immun
445	138	99.3	855	15	Q7SUS0	Q7sus0 human immun
446	138	99.3	855	15	Q7SUR9	Q7sur9 human immun
447	138	99.3	855	15	Q7SUR8	Q7sur8 human immun
448	138	99.3	855	15	Q7SUR7	Q7sur7 human immun
449	138	99.3	855	15	Q7SUR6	Q7sur6 human immun
450	138	99.3	855	15	Q7SUR5	Q7sur5 human immun
451	138	99.3	855	15	Q7SUR4	Q7sur4 human immun
452	138	99.3	855	15	Q7SUR1	Q7sur1 human immun
453	138	99.3	855	15	Q7SUR0	Q7sur0 human immun
454	138	99.3	855	15	Q7SII1	Q7si11 human immun
455	138	99.3	856	15	Q92873	Q92873 human immun
456	138	99.3	856	15	Q77694	Q77694 human immun
457	138	99.3	856	15	P90115	P90115 human immun
458	138	99.3	856	15	Q902G3	Q902g3 human immun
459	138	99.3	856	15	Q9WLH6	Q9wlh6 human immun
460	138	99.3	856	15	Q73297	Q73297 human immun
461	138	99.3	856	15	Q73293	Q73293 human immun
462	138	99.3	856	15	Q90079	Q90079 human immun
463	138	99.3	856	15	O8AD87	O8ad87 human immun
464	138	99.3	856	15	Q7ZJCO	Q7zjco human immun
465	138	99.3	856	15	Q8JDH5	Q8jdh5 human immun
466	138	99.3	857	15	Q8UL42	Q8ul42 human immun
467	138	99.3	857	15	Q8ULAO	Q8ulao human immun
468	138	99.3	857	15	Q8JDX7	Q8jdx7 human immun
469	138	99.3	857	15	O8UL89	O8ul89 human immun
470	138	99.3	857	15	O8ULP2	O8ulp2 human immun
471	138	99.3	857	15	O8AOS1	O8aos1 human immun
472	138	99.3	857	15	Q7ZJ87	Q7zj87 human immun
473	138	99.3	858	15	O92874	O92874 human immun
474	138	99.3	858	15	Q8Q865	Q8q865 human immun
475	138	99.3	858	15	O8UL75	O8ul75 human immun
476	138	99.3	858	15	Q8Q867	Q8q867 human immun
477	138	99.3	858	15	O8Q876	O8q876 human immun
478	138	99.3	858	15	O71974	O71974 human immun
479	138	99.3	858	15	Q73293	Q73293 human immun
480	138	99.3	858	15	Q9PY30	Q9py30 human immun
481	138	99.3	858	15	O56107	O56107 human immun
482	138	99.3	858	15	O8QD24	O8qdz4 human immun
483	138	99.3	858	15	Q7ZJE6	Q7zje6 human immun
484	138	99.3	858	15	Q7SVL1	Q7svl1 human immun
485	138	99.3	858	15	Q7SUT2	Q7sut2 human immun
486	138	99.3	859	15	Q8Q850	Q8q850 human immun
487	138	99.3	859	15	O8UPN8	O8upn8 human immun
488	138	99.3	859	15	O8UL77	O8ul77 human immun
489	138	99.3	859	15	Q9Q714	Q9q714 human immun
490	138	99.3	859	15	O92937	O92937 human immun
491	138	99.3	859	15	O11947	O11947 human immun
492	138	99.3	859	15	O8UL80	O8ul80 human immun
493	138	99.3	859	15	O8UL79	O8ul79 human immun
494	138	99.3	859	15	O8UL73	O8ul73 human immun
495	138	99.3	859	15	P87924	P87924 human immun
496	138	99.3	859	15	Q7SUT9	Q7sut9 human immun
497	138	99.3	859	15	Q7SUT8	Q7sut8 human immun
498	138	99.3	859	15	Q7SUT7	Q7sut7 human immun
499	138	99.3	859	15	Q7SUT6	Q7sut6 human immun
500	138	99.3	859	15	Q7SUT4	Q7sut4 human immun

ALIGNMENTS

RESULT 1

Q9YYZ9 PRELIMINARY; PRT; 117 AA.
AC Q9YYZ9
DT 01-MAY-1999 (T-EMBLrel. 10; Created)
DT 01-MAY-1999 (T-EMBLrel. 10; Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24; Last annotation update)
DE Gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=171.005;
RA Brennan C.A., Lund J.K., Golden A., Yamaguchi J., Vallari A.S.,
RA Phillips J.F., Kataaha P.K., Jackson J.B., Devare S.G.;
RT "Serologic and Phylogenetic Characterization of HIV-1 Subtypes in
RT Uganda.";
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF006876; AD01320.1; --
DR GO; GO:0016021; C:integral to membrane; IEA.


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DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1 1
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13970 MW; 480F82FC9AF0756D CRC64;

Query Match 100.0%; Score 139; DB 15; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.3e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLLGWCSGKLC 26
DB 23 RILAVERYLKDQQLLGWCSGKLC 48

RESULT 2
Q9YRU1 PRELIMINARY; PRT; 117 AA.
ID Q9YRU1 AC Q9YRU1
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=96USCM48;
RA Sullivan P.J., Do A., Ellenberger D.L., Pau C.-P., Paul S., Kalish M.,
RA Robbins K., Lal R., Storck C., Schable C.A., Wise H., Tetteh C.,
RA Jones J., Ward J.
RT "Surveillance of Central African Nationals living in the United States
RT reveals multiple subtypes of HIV-1 Group M and Group O."
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF096324; AAD04399.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1 1
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13986 MW; 4719FD6EB98E42E3 CRC64;

Query Match 100.0%; Score 139; DB 15; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.3e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLLGWCSGKLC 26
DB 19 RILAVERYLKDQQLLGWCSGKLC 44

RESULT 3
Q9QIU3 PRELIMINARY; PRT; 122 AA.
ID Q9QIU3 AC Q9QIU3
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=GP41ERRJ28;
RA Caride E., Hertogs K., Larder B., Dehertogh P., Brindeiro R.,
RA Machado E., de Sa C.A.M., Eyer W., Passioni L.F.C., Menezes J.A.,
RA Calazans A.R., Tanuri A.;
RT "Genotyping and phenotyping analysis of B and non-B Human
RT immunodeficiency virus type 1 subtypes from patients under HAART.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1 1
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 14817 MW; 8D6099E5D3993205 CRC64;

Query Match 100.0%; Score 139; DB 15; Length 122;
Best Local Similarity 100.0%; Pred. No. 1.4e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLLGWCSGKLC 26
DB 19 RILAVERYLKDQQLLGWCSGKLC 44

RESULT 4
Q9EA97 PRELIMINARY; PRT; 122 AA.
ID Q9EA97 AC Q9EA97
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BX404;
RX MEDLINE=20134570; PubMed=10669328;
RA Weidle P.J., Ganea C.E., Irwin K.L., Pieniazek D., McGowan J.P.,
RA Olivo N., Ramos A., Schable C., Lal R.B., Holmberg S.D., Ernst J.A.;
RT "Presence of human immunodeficiency virus (HIV) type 1, group M, non-B
RT subtypes, Bronx, New York: a sentinel site for monitoring HIV genetic
RT diversity in the United States.";
RL J. Infect. Dis. 181:470-475(2000).
DR EMBL; AF190955; AAG02317.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1 1
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 14763 MW; B9207B0EBE4213AA CRC64;

Query Match 100.0%; Score 139; DB 15; Length 122;
Best Local Similarity 100.0%; Pred. No. 1.4e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLLGWCSGKLC 26
DB 19 RILAVERYLKDQQLLGWCSGKLC 44

RESULT 5
Q9WQ23 PRELIMINARY; PRT; 122 AA.
ID Q9WQ23 AC Q9WQ23
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DT 01-NOV-1999 (TReMBLrel. 12, Created)
 DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
 DE Envelope glycoprotein (Fragment).
 GN ENV.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GH8;
 RA Pieniazek D., Yang C., Lal R.L.;
 RT "Phylogenetic analysis of gp41 envelope of HIV-1 groups M, N, and O isolates provides an alternate region for subtype determination.";
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF113589; AAD42757.1; -;
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0019031; C:viral envelope; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR000328; Env_GP41.
 DR Pfam; PF00517; GP41; 1.
 KW Transmembrane.
 FT NON_TER 1
 FT NON_TER 122
 SQ SEQUENCE 122 AA; 14703 MW; 09E2E31B37786D34 CRC64;
 Query Match 100.0%; Score 139; DB 15; Length 122;
 Best Local Similarity 100.0%; Pred. No. 1.4e-13;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RILAVERYLKDQQLGIWCSGKLC 26
 Db 19 RILAVERYLKDQQLGIWCSGKLC 44

RESULT 6
 QYXXP4
 ID Q9YXP4 PRELIMINARY; PRT; 122 AA.
 AC Q9YXP4;
 DT 01-MAY-1999 (TReMBLrel. 10, Created)
 DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
 DE Envelope glycoprotein immunodominant region (Fragment).
 GN ENV.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=RJ96BPF070;
 RA Tanuri A., Swanson P.A., Devare S.G., Berro O.J., Savedra A., Costa L.J., Telles J.G., Brindeiro R., Schable C., Pieniazek D., Rayfield M.;
 RT "HIV-1 subtypes among blood donors from Rio de Janeiro, Brazil.";
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF034059; RAC79311.1; -;
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0019031; C:viral envelope; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR000328; Env_GP41.
 DR Pfam; PF00517; GP41; 1.
 KW Transmembrane.
 FT NON_TER 1
 FT NON_TER 122
 SQ SEQUENCE 122 AA; 14819 MW; E3960B97ED1C08D6 CRC64;
 Query Match 100.0%; Score 139; DB 15; Length 122;
 Best Local Similarity 100.0%; Pred. No. 1.4e-13;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RILAVERYLKDQQLGIWCSGKLC 26
 Db 19 RILAVERYLKDQQLGIWCSGKLC 44

RESULT 7
 Q7ZJR4
 ID Q7ZJR4 PRELIMINARY; PRT; 122 AA.
 AC Q7ZJR4;
 DT 01-JUN-2003 (TReMBLrel. 24, Created)
 DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
 DE Envelope glycoprotein (Fragment).
 GN ENV.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=US4;
 RA Swanson P.A., Devare S.G., Hackett J.R. Jr.;
 RT "Molecular Characterization of 39 HIV-1 Isolates Representing Group M (Subtypes A-G) and Group O: Sequence Analysis of gag p24, pol integrase, and env gp41.";
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY214095; AAO61815.1; -;
 DR GO; GO:0019031; C:viral envelope; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR000328; Env_GP41.
 DR Pfam; PF00517; GP41; 1.
 KW Envelope protein.
 FT NON_TER 1
 FT NON_TER 122
 SQ SEQUENCE 122 AA; 14777 MW; AE2C9F40DF21CCFB CRC64;
 Query Match 100.0%; Score 139; DB 15; Length 122;
 Best Local Similarity 100.0%; Pred. No. 1.4e-13;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RILAVERYLKDQQLGIWCSGKLC 26
 Db 19 RILAVERYLKDQQLGIWCSGKLC 44

RESULT 8
 Q9AEX2
 ID Q9AEX2 PRELIMINARY; PRT; 123 AA.
 AC Q9AEX2;
 DT 01-MAR-2003 (TReMBLrel. 23, Created)
 DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
 DE Gp41 (Fragment).
 GN ENV.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Esteves A., Parreira R., Venenno T., Franco M., Piedade J., Germano de Sousa J., Canas-Ferreira W.;
 RT "Genetic diversity of HIV-1 spreading among intravenous drug users in Lisbon, Portugal.";
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ429041; CAD23677.1; -;
 DR GO; GO:0019031; C:viral envelope; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR000328; Env_GP41.
 DR Pfam; PF00517; GP41; 1.
 FT NON_TER 1
 FT NON_TER 123
 SQ SEQUENCE 123 AA; 14895 MW; 489C41C5C275D89F CRC64;
 Query Match 100.0%; Score 139; DB 15; Length 123;
 Best Local Similarity 100.0%; Pred. No. 1.4e-13;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 RILAVERYLKDQQLGIGCSGKLC 26
DB 17 RILAVERYLKDQQLGIGCSGKLC 42

RESULT 9
Q7ZCD7 Q7ZCD7 PRELIMINARY; PRT; 144 AA.
AC Q7ZCD7;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HRLUX53-1;
RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,
RA Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;
RT "Uncommon mutations at residue positions critical for enfuvirtide (T-
RT 20) resistance in enfuvirtide-naive patients infected with subtype B
RT and non-B HIV-1.";
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY185383; AAO65658.1; -.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Envelope protein.
FT NON_TER 1
FT NON_TER 144
SQ SEQUENCE 144 AA; 16887 MW; A139D1C53D18EBE CRC64;

Query Match 100.0%; Score 139; DB 15; Length 144;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIGCSGKLC 26
DB 50 RILAVERYLKDQQLGIGCSGKLC 75

RESULT 10
Q7ZCD6 Q7ZCD6 PRELIMINARY; PRT; 144 AA.
AC Q7ZCD6;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HRLUX53-2;
RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,
RA Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;
RT "Uncommon mutations at residue positions critical for enfuvirtide (T-
RT 20) resistance in enfuvirtide-naive patients infected with subtype B
RT and non-B HIV-1.";
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY185384; AAO65659.1; -.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Envelope protein.
FT NON_TER 1
FT NON_TER 144
SQ SEQUENCE 144 AA; 16887 MW; A139D1C53D18EBE CRC64;

Query Match 100.0%; Score 139; DB 15; Length 144;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIGCSGKLC 26
DB 50 RILAVERYLKDQQLGIGCSGKLC 75

RESULT 11
Q7ZC52 Q7ZC52 PRELIMINARY; PRT; 145 AA.
AC Q7ZC52;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HRLUX18;
RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,
RA Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;
RT "Uncommon mutations at residue positions critical for enfuvirtide (T-
RT 20) resistance in enfuvirtide-naive patients infected with B and non-B
RT subtype HIV-1.";
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY185468; AAO65743.1; -.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Envelope protein.
FT NON_TER 1
FT NON_TER 145
SQ SEQUENCE 145 AA; 17020 MW; AC8C32E97B09D1A1 CRC64;

Query Match 100.0%; Score 139; DB 15; Length 145;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIGCSGKLC 26
DB 48 RILAVERYLKDQQLGIGCSGKLC 73

RESULT 12
Q7ZC48 Q7ZC48 PRELIMINARY; PRT; 145 AA.
AC Q7ZC48;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HRLUX22;
RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,
RA Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;
RT "Uncommon mutations at residue positions critical for enfuvirtide (T-
RT 20) resistance in enfuvirtide-naive patients infected with B and non-B
RT subtype HIV-1.";
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
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GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA DCosta S.S., Hurwitz J.L.;
RT "Escape mutants to determine structure of gp120 of HIV-1.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF321147; AAK20295.1; -
DR PIR; A53591; A53591.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 588 588
SQ SEQUENCE 588 AA; 65643 MW; 47475A5780240AE8 CRC64;

Query Match 100.0%; Score 139; DB 15; Length 588;
Best Local Similarity 100.0%; Pred. No. 7e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGWCSGKLC 26
|||||
DB 522 RILAVERYLKDQQLGWCSGKLC 547

RESULT 17
Q993A7 PRELIMINARY; PRT; 588 AA.
AC Q993A7;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA DCosta S.S., Hurwitz J.L.;
RT "Escape mutants to determine structure of gp120 of HIV-1.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF321148; AAK20296.1; -
DR PIR; A53591; A53591.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 588 588
SQ SEQUENCE 588 AA; 65593 MW; 3FE7610B592EFC6D CRC64;

Query Match 100.0%; Score 139; DB 15; Length 588;
Best Local Similarity 100.0%; Pred. No. 7e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGWCSGKLC 26
|||||
DB 522 RILAVERYLKDQQLGWCSGKLC 547

RESULT 18
Q993B1 PRELIMINARY; PRT; 589 AA.
AC Q993B1;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA DCosta S.S., Hurwitz J.L.;
RT "Escape mutants to determine structure of gp120 of HIV-1.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF321144; AAK20292.1; -
DR PIR; A53591; A53591.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 589 589
SQ SEQUENCE 589 AA; 65753 MW; 00621646924FD66 CRC64;

Query Match 100.0%; Score 139; DB 15; Length 589;
Best Local Similarity 100.0%; Pred. No. 7e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGWCSGKLC 26
|||||
DB 522 RILAVERYLKDQQLGWCSGKLC 547

RESULT 19
Q993A9 PRELIMINARY; PRT; 590 AA.
AC Q993A9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=wt2;
RA DCosta S.S., Hurwitz J.L.;
RT "Escape mutants to determine structure of gp120 of HIV-1.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF321146; AAK20294.1; -
DR PIR; A53591; A53591.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 590 590
SQ SEQUENCE 590 AA; 65753 MW; 00621646924FD66 CRC64;

Query Match 100.0%; Score 139; DB 15; Length 589;
Best Local Similarity 100.0%; Pred. No. 7e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGWCSGKLC 26
|||||
DB 522 RILAVERYLKDQQLGWCSGKLC 547
```

```
FT NON_TER 1 1
FT NON_TER 590 590
SQ SEQUENCE 590 AA; 65902 MW; 91ED899CB8F91CAF CRC64;

Query Match 100.0%; Score 139; DB 15; Length 590;
Best Local Similarity 100.0%; Pred. No. 7e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSGKLIC 26
|||||
Db 523 RILAVERYLKDQQLGIWCGSGKLIC 548

RESULT 20
Q993B0 PRELIMINARY; PRT; 616 AA.
AC Q993B0;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1H6;
RA DCosta S.S., Hurwitz J.L.;
RT "Escape mutants to determine structure of gp120 of HIV-1.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF321145; AAK20293.1; -.
DR PIR; A53591; A53591.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR Pfam; PF00517; GP120.
DR Aids; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
KW NON_TER 1
FT NON_TER 616
SQ SEQUENCE 616 AA; 69189 MW; 57A8E20F9A580A4F CRC64;

Query Match 100.0%; Score 139; DB 15; Length 616;
Best Local Similarity 100.0%; Pred. No. 7.3e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSGKLIC 26
|||||
Db 523 RILAVERYLKDQQLGIWCGSGKLIC 548

RESULT 21
Q993B2 PRELIMINARY; PRT; 618 AA.
AC Q993B2;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1B6;
RA DCosta S.S., Hurwitz J.L.;
RT "Escape mutants to determine structure of gp120 of HIV-1.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
```

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DR EMBL; AF321143; AAK20291.1; -.
DR PIR; A53591; A53591.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW Aids; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 618
SQ SEQUENCE 618 AA; 69364 MW; B9C791E7D357D2AE CRC64;

Query Match 100.0%; Score 139; DB 15; Length 618;
Best Local Similarity 100.0%; Pred. No. 7.3e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSGKLIC 26
|||||
Db 525 RILAVERYLKDQQLGIWCGSGKLIC 550

RESULT 22
Q90723 PRELIMINARY; PRT; 727 AA.
AC Q90723;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Envelope polyprotein variant.
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=11IBX;
RX MEDLINE=93272698; PubMed=10339592;
RA Hofman T.L., LaBranche C.C., Zhang W., Canziani G., Robinson J.,
RA Chaiken I., Hoxie J.A., Doms R.W.;
RT "Stable exposure of the coreceptor-binding site in a CD4-independent
RT HIV-1 envelope protein.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:6359-6364 (1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=11IBX;
RX MEDLINE=20027260; PubMed=10559349;
RA LaBranche C.C., Hoffman T.L., Romano J., Haggarty B.S., Edwards T.G.,
RA Matthews T.J., Doms R.W., Hoxie J.A.;
RT "Determinants of CD4 independence for a human immunodeficiency virus
RT type 1 variant map outside regions required for coreceptor
RT specificity.";
RL J. Virol. 73:10310-10319 (1999).
DR EMBL; AF189158; AAF25627.1; -.
DR PIR; A53591; A53591.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW Aids; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
SQ SEQUENCE 727 AA; 82201 MW; F90FD626D26B9E66 CRC64;

Query Match 100.0%; Score 139; DB 15; Length 727;
Best Local Similarity 100.0%; Pred. No. 8.7e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSGKLIC 26
```

Db 574 RILAVERYLKDQQLGWCCKLIC 599
|||||

RESULT 23

Q70607 PRELIMINARY; PRT; 747 AA.
AC Q70607;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LW87-1;
RX MEDLINE=95127297; PubMed=7826699;
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
RA Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;
RT "viral variability and serum antibody response in a laboratory worker
RT infected with HIV type 1 (HTLV type IIIB).";
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=LW87-1;
RA Mulder K.E.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U12034; AAA76669.1; -.
DR PIR; A53591; A53591.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 747
SQ SEQUENCE 747 AA; 84250 MW; 732B836A52245F14 CRC64;

Query Match 100.0%; Score 139; DB 15; Length 747;
Best Local Similarity 100.0%; Pred. No. 8.9e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGWCCKLIC 26
|||||

Db 574 RILAVERYLKDQQLGWCCKLIC 599
|||||

RESULT 24

Q70606 PRELIMINARY; PRT; 748 AA.
AC Q70606;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LW881;
RX MEDLINE=95127297; PubMed=7826699;
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
RA Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;
RT "viral variability and serum antibody response in a laboratory worker
RT infected with HIV type 1 (HTLV type IIIB).";

RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=LW881;
RA Mulder K.E.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U12032; AAA76668.1; -.
DR PIR; A53591; A53591.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 748
SQ SEQUENCE 748 AA; 84224 MW; 56BEDF186C67694B CRC64;

Query Match 100.0%; Score 139; DB 15; Length 748;
Best Local Similarity 100.0%; Pred. No. 9e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGWCCKLIC 26
|||||

Db 575 RILAVERYLKDQQLGWCCKLIC 600
|||||

RESULT 25

Q70604 PRELIMINARY; PRT; 752 AA.
ID Q70604;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LW851;
RX MEDLINE=95127297; PubMed=7826699;
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
RA Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;
RT "viral variability and serum antibody response in a laboratory worker
RT infected with HIV type 1 (HTLV type IIIB).";
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=LW851;
RA Mulder K.E.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U12030; AAA76666.1; -.
DR PIR; A53591; A53591.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 752
SQ SEQUENCE 752 AA; 84894 MW; 8B30AE894013B45A CRC64;

Query Match 100.0%; Score 139; DB 15; Length 752;
Best Local Similarity 100.0%; Pred. No. 9e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 RILAVERYLKDQQLGIWCSGKLIC 26
Db 579 RILAVERYLKDQQLGIWCSGKLIC 604

RESULT 26
Q70605 PRELIMINARY; PRT; 752 AA.
AC Q70605;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LW852;
RX MEDLINE=95127297; PubMed=7826699;
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
RA Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;
RT "Viral variability and serum antibody response in a laboratory worker
RT infected with HIV type 1 (HTLV type IIIB).";
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=LW852;
RA Mulder K.E.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U12031; AAA76667.1; -.
DR PIR; A53591; A53591.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 752 752
SQ SEQUENCE 752 AA; 84894 MW; 8B30AB894013B45A CRC64;

Query Match 100.0%; Score 139; DB 15; Length 752;
Best Local Similarity 100.0%; Pred. No. 9e-13; Mismatches 0; Indels 0; Gaps 0;
Matches 26; Conservative 0;

QY 1 RILAVERYLKDQQLGIWCSGKLIC 26
Db 579 RILAVERYLKDQQLGIWCSGKLIC 604

RESULT 27
Q70608 PRELIMINARY; PRT; 752 AA.
AC Q70608;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LW87-2;
RX MEDLINE=95127297; PubMed=7826699;
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
RA Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;
RT "Viral variability and serum antibody response in a laboratory worker
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RX Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
RA Nzilambi N., Apetrei C., Ekwilanga M., Delaporte E., Peeters M.;
RT "High diversity of HIV-1 subtype F strains in Central Africa.";
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
SQ SEQUENCE 757 AA; 85539 MW; A759AF8D8263BD2E CRC64;

Query Match 100.0%; Score 139; DB 15; Length 757;
Best Local Similarity 100.0%; Pred. No. 9.1e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGWCSCGKLC 26
DB 574 RILAVERYLKDQQLGWCSCGKLC 559

RESULT 29
Q9WMV1 PRELIMINARY; PRT; 800 AA.
AC Q9WMV1;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope (Gp160) (Fragment).
GN ENV OR GP160.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MP255;
RX MEDLINE=99294894; PubMed=10364493;
RA Triques K., Bourgeois A., Saragosti S., Vidal N., Mpoudi-Ngole E.,
RA Nzilambi N., Apetrei C., Ekwilanga M., Delaporte E., Peeters M.;
RT "High diversity of HIV-1 subtype F strains in Central Africa.";
RL Virology 259:99-109 (1999).
DR EMBL; AJ237805; CAB44056.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 800
SQ SEQUENCE 800 AA; 90612 MW; 79A7EA536AFAPFC1 CRC64;

Query Match 100.0%; Score 139; DB 15; Length 800;
Best Local Similarity 100.0%; Pred. No. 9.1e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGWCSCGKLC 26
DB 533 RILAVERYLKDQQLGWCSCGKLC 558

RESULT 30
Q9WMU9 PRELIMINARY; PRT; 801 AA.
AC Q9WMU9;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope (Gp160) (Fragment).
GN ENV OR GP160.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MP535;
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RX MEDLINE=99294894; PubMed=10364493;
RA Triques K., Bourgeois A., Saragosti S., Vidal N., Mpoudi-Ngole E.,
RA Nzilambi N., Apetrei C., Ekwilanga M., Delaporte E., Peeters M.;
RT "High diversity of HIV-1 subtype F strains in Central Africa.";
RL Virology 259:99-109 (1999).
DR EMBL; AJ237807; CAB44058.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 801
SQ SEQUENCE 801 AA; 90521 MW; 9AE71C1C840A88B CRC64;

Query Match 100.0%; Score 139; DB 15; Length 801;
Best Local Similarity 100.0%; Pred. No. 9.6e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGWCSCGKLC 26
DB 534 RILAVERYLKDQQLGWCSCGKLC 559

RESULT 31
Q8Q2X2 PRELIMINARY; PRT; 807 AA.
AC Q8Q2X2;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein.
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Gorry P.R., Taylor J., Holm G., Mehle A., Morgan T., Cayabyab M.,
RA Farzan M., Wang H., Bell J.B., Kunstman K.J., Moore J.P.,
RA Wolinsky S.M., Gabuzda D.;
RT "Increased CCR5 affinity and reduced CCR5/CD4 dependence of a
RT neurovirulent primary human immunodeficiency virus type 1 isolate.";
RL J. Virol. 0:0-0 (2002).
DR EMBL; AF491740; AAM09793.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
SQ SEQUENCE 807 AA; 91808 MW; 4B52479155EF5603 CRC64;

Query Match 100.0%; Score 139; DB 15; Length 807;
Best Local Similarity 100.0%; Pred. No. 9.7e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGWCSCGKLC 26
DB 590 RILAVERYLKDQQLGWCSCGKLC 615

RESULT 32
Q9WMV0 PRELIMINARY; PRT; 809 AA.
AC Q9WMV0;
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DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope (Gp160) (Fragment)
GN ENV OR Gp160
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
[1]
RN RP SEQUENCE FROM N.A.
RC STRAIN=MP257;
EX MEDLINE=99294894; PubMed=10364493;
RA Triques K., Bourgeois A., Saragosti S., Vidal N., Mpoudi-Etong E.,
RA Nzilambi N., Apetret C., Ekwilanga M., Delaporte E., Peeters M.;
RT "High diversity of HIV-1 subtype F strains in Central Africa.";
RL Virology 259:99-109 (1999).
DR EMBL: AJ237806; CAB44057.1; -.
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0019028; C: viral capsid; IEA.
DR GO: GO:0019031; C: viral envelope; IEA.
DR GO: GO:0005198; F: structural molecule activity; IEA.
DR InterPro: IPR000328; Env GP41.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 809
SQ SEQUENCE 809 AA; 91516 MW; 24F5179F72B08F1A CRC64;
Query Match 100.0%; Score 139; DB 15; Length 809;
Best Local Similarity 100.0%; Pred. No. 9.7e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RILAVERYLKDQQLGIWCGSKLIC 26
Db 542 RILAVERYLKDQQLGIWCGSKLIC 567
RESULT 33
Q9DVL1
ID Q9DVL1 PRELIMINARY; PRT; 826 AA.
AC Q9DVL1;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope protein (Fragment).
GN ENV OR Gp160.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
[1]
RN RP SEQUENCE FROM N.A.
RC STRAIN=97DC.KTB22;
EX MEDLINE=20499072; PubMed=11044094;
RA Vidal N., Peeters M., Mulanga-Kabeya C., Nzilambi N., Robertson D.,
RA Ilunga W., Sema H., Tshimanga K., Bongo B., Delaporte E.;
RT "Unprecedented degree of human immunodeficiency virus Type 1 (HIV-1)
RT group M genetic diversity in the Democratic Republic of Congo suggests
RT that the HIV-1 pandemic originated in Central Africa.";
RL J. Virol. 74:10498-10507 (2000).
DR EMBL: AJ401042; CAC15050.1; -.
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0019028; C: viral capsid; IEA.
DR GO: GO:0019031; C: viral envelope; IEA.
DR GO: GO:0005198; F: structural molecule activity; IEA.
DR InterPro: IPR000328; Env GP41.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 826
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SQL SEQUENCE 826 AA; 93694 MW; 344AF31B694B6883 CRC64;
Query Match 100.0%; Score 139; DB 15; Length 826;
Best Local Similarity 100.0%; Pred. No. 9.9e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RILAVERYLKDQQLGIWCGSKLIC 26
Db 566 RILAVERYLKDQQLGIWCGSKLIC 591
RESULT 34
Q9ID89
ID Q9ID89 PRELIMINARY; PRT; 845 AA.
AC Q9ID89;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE ENV protein.
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
[1]
RN RP SEQUENCE FROM N.A.
RC STRAIN=95127;
RA Montavon C., Delaporte E., Peeters M.;
RT "Two new complete genomes of HIV-1 recombinant AGU BPP90-like
RT circulating in Mali and Senegal.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ288982; CAB98175.1; -.
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0019028; C: viral capsid; IEA.
DR GO: GO:0019031; C: viral envelope; IEA.
DR GO: GO:0005198; F: structural molecule activity; IEA.
DR InterPro: IPR000328; Env GP41.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
SQ SEQUENCE 845 AA; 95239 MW; 39439B37713EBD2A CRC64;
Query Match 100.0%; Score 139; DB 15; Length 845;
Best Local Similarity 100.0%; Pred. No. 1e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RILAVERYLKDQQLGIWCGSKLIC 26
Db 568 RILAVERYLKDQQLGIWCGSKLIC 593
RESULT 35
Q69996
ID Q69996 PRELIMINARY; PRT; 847 AA.
AC Q69996;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
[1]
RN RP SEQUENCE FROM N.A.
RC STRAIN=594;
EX MEDLINE=96190564; PubMed=8627686;
RA Gao F., Morrison S.G., Robertson D.L., Thornton C.L., Craig S.,
RA Karlsson G., Sodroski J., Morgado M., Galvao-Castro B.,
RA von Briesen H., Beddows S., Weber J., Sharp P.M., Shaw G.M.,
RA Hahn B.H.;
RT "Molecular cloning and analysis of functional envelope genes from
RT human immunodeficiency virus type 1 sequence subtypes A through G. The
```

RT WHO and NIAID Networks for HIV Isolation and Characterization.";
RL J. Virol. 70:1651-1657(1996).
RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=594;
RA NIAID/NIH DAIDS Variation Program;

RL Submitted (MAY-1994) to the EMBL/GenBank/DBJ databases.
RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=594;
RA McEvilly M.M.;

RL Submitted (APR-1994) to the EMBL/GenBank/DBJ databases.
RN [2]

RC STRAIN=594;
RA McEvilly M.M.;

RL Submitted (APR-1994) to the EMBL/GenBank/DBJ databases.
RN [2]

RC STRAIN=594;
RA McEvilly M.M.;

RL Submitted (APR-1994) to the EMBL/GenBank/DBJ databases.
RN [2]

RC STRAIN=594;
RA McEvilly M.M.;

RL Submitted (APR-1994) to the EMBL/GenBank/DBJ databases.
RN [2]

RC STRAIN=594;
RA McEvilly M.M.;

RL Submitted (APR-1994) to the EMBL/GenBank/DBJ databases.
RN [2]

RC STRAIN=594;
RA McEvilly M.M.;

RL Submitted (APR-1994) to the EMBL/GenBank/DBJ databases.
RN [2]

RC STRAIN=594;
RA McEvilly M.M.;

RL Submitted (APR-1994) to the EMBL/GenBank/DBJ databases.
RN [2]

RC STRAIN=594;
RA McEvilly M.M.;

RL Submitted (APR-1994) to the EMBL/GenBank/DBJ databases.
RN [2]

RC STRAIN=594;
RA McEvilly M.M.;

RL Submitted (APR-1994) to the EMBL/GenBank/DBJ databases.
RN [2]

RC STRAIN=594;
RA McEvilly M.M.;

RL Submitted (APR-1994) to the EMBL/GenBank/DBJ databases.
RN [2]

RC STRAIN=594;
RA McEvilly M.M.;

RL Submitted (APR-1994) to the EMBL/GenBank/DBJ databases.
RN [2]

RC STRAIN=594;
RA McEvilly M.M.;

RL Submitted (APR-1994) to the EMBL/GenBank/DBJ databases.
RN [2]

RC STRAIN=594;
RA McEvilly M.M.;

RL Submitted (APR-1994) to the EMBL/GenBank/DBJ databases.
RN [2]

RC STRAIN=594;
RA McEvilly M.M.;

RL Submitted (APR-1994) to the EMBL/GenBank/DBJ databases.
RN [2]

RC STRAIN=594;
RA McEvilly M.M.;

RL Submitted (APR-1994) to the EMBL/GenBank/DBJ databases.
RN [2]

RC STRAIN=594;
RA McEvilly M.M.;

RL Submitted (APR-1994) to the EMBL/GenBank/DBJ databases.
RN [2]

RC STRAIN=594;
RA McEvilly M.M.;

RL Submitted (APR-1994) to the EMBL/GenBank/DBJ databases.
RN [2]

RC STRAIN=594;
RA McEvilly M.M.;

RL Submitted (APR-1994) to the EMBL/GenBank/DBJ databases.
RN [2]

RC STRAIN=594;
RA McEvilly M.M.;

RL Submitted (APR-1994) to the EMBL/GenBank/DBJ databases.
RN [2]

RC STRAIN=594;
RA McEvilly M.M.;

RL Submitted (APR-1994) to the EMBL/GenBank/DBJ databases.
RN [2]

RC STRAIN=594;
RA McEvilly M.M.;

RL Submitted (APR-1994) to the EMBL/GenBank/DBJ databases.
RN [2]

RC STRAIN=594;
RA McEvilly M.M.;

RL Submitted (APR-1994) to the EMBL/GenBank/DBJ databases.
RN [2]

RC STRAIN=594;
RA McEvilly M.M.;

RT "Molecular cloning and phylogenetic analysis of human immunodeficiency
 RT virus type 1 subtype C: a set of 23 full-length clones from
 RT Botswana.";
 RL J. Virol. 73:4427-4432(1999).
 RN [2]

RP SEQUENCE FROM N.A.
 RC STRAIN=C-96BW05.04;
 RA Novitsky V.A., Montano M.A., McLane M.F., Renjifo B., Vannberg F.,
 RA Foley B.T., Ndung'u T.P., Marlink R., Essex M.;
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF110968; A017084.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0019028; C:viral capsid; IEA.
 DR GO; GO:0019031; C:viral envelope; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR000328; Env_GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
 SQ SEQUENCE 849 AA; 96310 MW; 32747D3CCE098D1 CRC64;

Query Match 100.0%; Score 139; DB 15; Length 849;
 Best Local Similarity 100.0%; Pred. No. 1e-12;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RILAVERYLKDQQLGIWCGSKLIC 26

Db 572 RILAVERYLKDQQLGIWCGSKLIC 597

RESULT 39

OQ0BY2 PRELIMINARY; PRT; 850 AA.
 AC Q0BY2
 DT 01-MAY-2000 (TRENBLrel. 13, Created)
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
 DE ENV protein (Fragment).
 GN ENV
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=96CM-MP535;
 RX MEDLINE=2012179; PubMed=10659053;
 RA Triques K., Bourgeois A., Vidale N., Mpoudi-Ngole E.,
 RA Mulanga-Kabeya C., Nzilambi N., Torimiro N., Saman E., Delaporte E.,
 RA Peeters M.;
 RL "Near-full-length genome sequencing of divergent African HIV type 1
 RT subtype F viruses leads to the identification of a new HIV type 1
 RT subtype designated K.";
 RL AIDS Res. Hum. Retroviruses 16:139-151(2000).
 DR EMBL; AJ249239; CAB58990.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0019028; C:viral capsid; IEA.
 DR GO; GO:0019031; C:viral envelope; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR000328; Env_GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
 FT CHAIN 842 850 NEF PROTEIN.
 SQ SEQUENCE 850 AA; 96145 MW; 04B8B7B30E7307CE CRC64;

Query Match 100.0%; Score 139; DB 15; Length 850;
 Best Local Similarity 100.0%; Pred. No. 1e-12;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RILAVERYLKDQQLGIWCGSKLIC 26

Db 573 RILAVERYLKDQQLGIWCGSKLIC 598

RESULT 40

OQ0BZ4 PRELIMINARY; PRT; 851 AA.
 AC Q0BZ4
 DT 01-MAY-2000 (TRENBLrel. 13, Created)
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
 DE ENV protein (Fragment).
 GN ENV
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=95CM-MP255;
 RX MEDLINE=2012179; PubMed=10659053;
 RA Triques K., Bourgeois A., Vidale N., Mpoudi-Ngole E.,
 RA Mulanga-Kabeya C., Nzilambi N., Torimiro N., Saman E., Delaporte E.,
 RA Peeters M.;
 RL "Near-full-length genome sequencing of divergent African HIV type 1
 RT subtype F viruses leads to the identification of a new HIV type 1
 RT subtype designated K.";
 RL AIDS Res. Hum. Retroviruses 16:139-151(2000).
 DR EMBL; AJ249236; CAB58978.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0019028; C:viral capsid; IEA.
 DR GO; GO:0019031; F:structural molecule activity; IEA.
 DR InterPro; IPR000328; Env_GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
 FT NON_TER 1 851 NEF PROTEIN.
 FT CHAIN 843 851
 SQ SEQUENCE 851 AA; 96591 MW; 1FA238916F5F8A96 CRC64;

Query Match 100.0%; Score 139; DB 15; Length 851;
 Best Local Similarity 100.0%; Pred. No. 1e-12;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RILAVERYLKDQQLGIWCGSKLIC 26

Db 574 RILAVERYLKDQQLGIWCGSKLIC 599

RESULT 41

O56566 PRELIMINARY; PRT; 854 AA.
 AC O56566;
 DT 01-JUN-1998 (TRENBLrel. 06, Created)
 DT 01-JUN-1998 (TRENBLrel. 06, Last sequence update)
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
 DE Envelope glycoprotein.
 GN ENV
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PH309;
 RX MEDLINE=99372987; PubMed=10445815;
 RA Ataman-Onal Y., Coiffier C., Giraud A., Babic-Erceg A., Biron F.,
 RA Verrier B.;
 RL "Comparison of complete env gene sequences from individuals with
 RT symptomatic primary HIV type 1 infection.";
 RL AIDS Res. Hum. Retroviruses 15:1035-1039(1999).
 DR EMBL; AF041132; AAC02523.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.

```
DR GO: GO:0019028; C:viral capsid; IEA.
DR GO: GO:0019031; C:viral envelope; IEA.
DR GO: GO:0005198; F:structural molecule activity; IEA.
DR InterPro: IPR000328; Env GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
SQ SEQUENCE 854 AA; 97062 MW; 58B012C83A0C3DA2 CRC64;

Query Match 100.0%; Score 139; DB 15; Length 854;
Best Local Similarity 100.0%; Pred. No. 1e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLLGWCSGKLIC 26
Db 577 RILAVERYLKDQQLLGWCSGKLIC 602

RESULT 42
Q85582 PRELIMINARY; PRT; 854 AA.
AC Q85582;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope polyprotein.
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86281827; PubMed=3016298;
RA Adachi A., Gendelman H.E., Koenig S., Folks T., Willey R., Rabson A.,
RA Martin M.A.;
RT "Production of acquired immunodeficiency syndrome-associated
RT retrovirus in human and nonhuman cells transfected with an infectious
RT molecular clone.";
RL J. Virol. 59:284-291(1986).
RN [2]
RP SEQUENCE FROM N.A.
RA Buckler C.E., Buckler-White A.J., Willey R.L., McCoy J.;
RL Submitted (JUL-1989) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Buckler C.E.;
RL Submitted (JUL-1989) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=92219406; PubMed=1373204;
RA Dai L.C., Littau R., Takahashi K., Ennis F.A.;
RT "Mutation of human immunodeficiency virus type 1 at amino acid 585 on
RT gp41 results in loss of killing by CD8+ A24-restricted cytotoxic T
RT lymphocytes.";
RL J. Virol. 66:3151-3154(1992).
DR EMBL: M19921; AAA44992.1; -.
DR PIR: A53591; A53591.
DR PIR: S13288; S13288.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0019028; C:viral capsid; IEA.
DR GO: GO:0019031; C:viral envelope; IEA.
DR GO: GO:0005198; F:structural molecule activity; IEA.
DR InterPro: IPR000328; Env GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
SQ SEQUENCE 854 AA; 97124 MW; ABA0A1BF36D5595A CRC64;

Query Match 100.0%; Score 139; DB 15; Length 854;
Best Local Similarity 100.0%; Pred. No. 1e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 RILAVERYLKDQQLLGWCSGKLIC 26
Db 577 RILAVERYLKDQQLLGWCSGKLIC 602

RESULT 43
Q8UNL0 PRELIMINARY; PRT; 854 AA.
AC Q8UNL0;
DT 01-WAR-2002 (TrEMBLrel. 20, Created)
DT 01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein.
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=X623;
RA Delgado E., Thomson M.M., Villahermosa M.L., Sierra M., Ocampo A.,
RA Miralles C., Rodriguez-Perez R., Diz-Aren J., Ojea-de-Castro R.,
RA Losada E., Cuevas M.T., Vazquez de Parga E., Carmona R.,
RA Perez Alvarez L., Medrano L., Cuevas L., Taboada J.A., Najera R.;
RT "Identification of a newly characterized HIV-1 BG intersubtype
RT circulating Recombinant Form in Galicia, Spain, exhibiting a
RT pseudotype-like virion structure.";
RL J. Acquir. Immune Defic. Syndr. 0:0-0(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=X623;
RA Delgado E., Thomson M.M., Villahermosa M.L., Sierra M., Ocampo A.,
RA Miralles C., Rodriguez-Perez R., Diz-Aren J., Ojea-de-Castro R.,
RA Losada E., Cuevas M.T., Vazquez de Parga E., Carmona R.,
RA Perez Alvarez L., Medrano L., Cuevas L., Taboada J.A., Najera R.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF450097; AAL47042.1; -.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0019028; C:viral capsid; IEA.
DR GO: GO:0019031; C:viral envelope; IEA.
DR GO: GO:0005198; F:structural molecule activity; IEA.
DR InterPro: IPR000328; Env GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
SQ SEQUENCE 854 AA; 96484 MW; 0661AA61D8DFC7C8 CRC64;

Query Match 100.0%; Score 139; DB 15; Length 854;
Best Local Similarity 100.0%; Pred. No. 1e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLLGWCSGKLIC 26
Db 570 RILAVERYLKDQQLLGWCSGKLIC 595

RESULT 44
Q72502 PRELIMINARY; PRT; 854 AA.
AC Q72502;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE ENV polyprotein.
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NL4-3;
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DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
SQ SEQUENCE 854 AA; 96885 MW; 0808F3AED27C693B CRC64;

Query Match 100.0%; Score 139; DB 15; Length 854;
Best Local Similarity 100.0%; Pred. No. 1e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIIC 26
DB 577 RILAVERYLKDQQLGIWGCSGKLIIC 602

RESULT 46
QSDVL2 PRELIMINARY; PRT; 854 AA.
AC Q9DVL2
AC Q9DVL2;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope protein (Fragment).
GN ENV OR GP160.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=J 97DC.KTB147;
RX MEDLINE=30495072; PubMed=11044094;
RA Iiduna W., Peeters M., Mlunga-Kabeya C., Nzilambi N., Robertson D.,
RA Ilunga W., Sema H., Tshimanga K., Bongo B., Delaporte E.;
RT group M genetic diversity in the Democratic Republic of Congo suggests
RT that the HIV-1 pandemic originated in Central Africa.";
RL Virol. 74:10498-10507(2000).
DR ENBL; AJ401041; CAC15049.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON TER 1
SQ SEQUENCE 854 AA; 96040 MW; 5A13A29231B0EDCF CRC64;

Query Match 100.0%; Score 139; DB 15; Length 854;
Best Local Similarity 100.0%; Pred. No. 1e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIIC 26
DB 577 RILAVERYLKDQQLGIWGCSGKLIIC 602

RESULT 47
Q78705 PRELIMINARY; PRT; 854 AA.
ID Q78705
AC Q78705;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein gp120.
GN ENV.
OC Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

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OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96013815; PubMed=7474132;
RA Duensing T.D., Fang H., Dorward D.W., Pincus S.H.;
RT "Processing of the envelope glycoprotein gp160 in immunotoxin-
RT resistant cell lines chronically infected with human immunodeficiency
RT virus type 1.";
RL J. Virol. 69:7122-7131(1995).
DR EMBL; L42371; AAA96326.1; -.
DR PIR; A53591; A53591.
DR PIR; S13288; S13288.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
SQ SEQUENCE 854 AA; 97199 MW; 5B9512216533E256 CRC64;
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
SQ
Query Match 100.0%; Score 139; DB 15; Length 854;
Best Local Similarity 100.0%; Pred. No. 1e-12; Indels 0; Gaps 0;
Matches 26; Conservative 0; Mismatches 0;
QY 1 RILAVERYLKDQQLGIWCSGKLLC 26
|||||
DB 577 RILAVERYLKDQQLGIWCSGKLLC 602
RESULT 48
Q8AQV7
ID Q8AQV7 PRELIMINARY; PRT; 855 AA.
AC Q8AQV7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein.
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Lemey P., Salemi M., Wang B., Saksena N.K., Vandamme A.M.;
RT "Maximum Likelihood Analysis of Clock-Like Behavior in HIV:
RT Implications on Dating Strategies in HIV Molecular Phylogenies.";
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF538302; AAN64079.1; -.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
SQ SEQUENCE 855 AA; 97180 MW; 81887BBFAD516F27 CRC64;
Query Match 100.0%; Score 139; DB 15; Length 855;
Best Local Similarity 100.0%; Pred. No. 1e-12; Indels 0; Gaps 0;
Matches 26; Conservative 0; Mismatches 0;
QY 1 RILAVERYLKDQQLGIWCSGKLLC 26
|||||
DB 578 RILAVERYLKDQQLGIWCSGKLLC 603
RESULT 49
Q74090
ID Q74090 PRELIMINARY; PRT; 856 AA.
AC Q74090;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Env.
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PM213;
RX MEDLINE=90101366; PubMed=1688473;
RA Cloud M.W., Moore B.E.;
RT "Spectrum of Biological Properties of Human Immunodeficiency Virus
RT (HIV-1) Isolates.";
RL Virology 174:103-116(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=PM213;
RA Iwatani Y.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; D86069; BAA13003.1; -.
DR PIR; A53591; A53591.
DR PIR; S13288; S13288.
DR PDB; 1F23; 20-JUN-01.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
SQ SEQUENCE 856 AA; 97396 MW; FE3E784C423C108C CRC64;
Query Match 100.0%; Score 139; DB 15; Length 856;
Best Local Similarity 100.0%; Pred. No. 1e-12; Indels 0; Gaps 0;
Matches 26; Conservative 0; Mismatches 0;
QY 1 RILAVERYLKDQQLGIWCSGKLLC 26
|||||
DB 579 RILAVERYLKDQQLGIWCSGKLLC 604
RESULT 50
O92877
ID O92877 PRELIMINARY; PRT; 856 AA.
AC O92877;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein.
GN ENV.
OS Simian-Human immunodeficiency virus.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=57667;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99098984; PubMed=9882298;
RA Cayabyab M., Karlsson G.B., Etemad-Moghadam B.A., Hofmann W.,
RA Steenbeke T., Halloran M., Fantom J.W., Axthelm M.K., Letvin N.L.,
RA Sodroski J.G.;
RT "Changes in human immunodeficiency virus type 1 envelope glycoproteins
RT responsible for the pathogenicity of a multiply passaged simian-human
RT immunodeficiency virus (SHIV-HXB2).";
RL J. Virol. 73:976-984(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Cayabyab M., Karlsson G.B., Etemad-Moghadam B., Hofmann W.,
RA Halloran M., Axthelm M.W., Letvin N.L., Sodroski J.G.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF041850; AAD12142.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
SQ SEQUENCE 856 AA; 97151 MW; C50BE0388PB73659 CRC64;

Query Match 100.0%; Score 139; DB 15; Length 856;
Best Local Similarity 100.0%; Pred. No. 1e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCGSKLIC 26
|||||
DB 579 RILAVERYLKDQQLGIWGCGSKLIC 604

RESULT 51

Q74599 PRELIMINARY; PRT; 856 AA.
AC O74599;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Env.
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MCK1;
RX MEDLINE=90101366; PubMed=1688473;
RA Cloyd M.W., Moore B.E.;
RT "Spectrum of Biological Properties of Human Immunodeficiency Virus
(HIV-1) Isolates.";
RT Virology 174:103-116(1990).
RN [2]

RP SEQUENCE FROM N.A.
RC STRAIN=MCK1;
RA Iwatani Y.;

RL Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
DR EMBL; D86088; BAA12995.1; -.
DR PIR; A53591; A53591.
DR PIR; S13288; S13288.
DR PDB; 1F23; 20-JUN-01.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
SQ SEQUENCE 856 AA; 97287 MW; 238042A234C56685 CRC64;

Query Match 100.0%; Score 139; DB 15; Length 856;
Best Local Similarity 100.0%; Pred. No. 1e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCGSKLIC 26
|||||
DB 579 RILAVERYLKDQQLGIWGCGSKLIC 604

RESULT 52

O92822 PRELIMINARY; PRT; 857 AA.
AC O92822;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)

DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein.
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ACH168.10;
RX MEDLINE=95074890; PubMed=7983734;
RA Wrin T., Loh T.P., Vennart J.C., Schuitemaker H., Nunberg J.H.;
RT "Adaptation to persistent growth in the H9 cell line renders a primary
isolate of human immunodeficiency virus type 1 sensitive to
neutralization by vaccine sera.";
RL J. Virol. 69:39-48(1995).
RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=ACH168.10;
RA LaCasse R.A., Follis K.E., Moudgil T., Trahey M., Binley J.M.,
RA Planellies V., Zolla-Pazner S., Nunberg J.H.;
RT "Coreceptor utilization by human immunodeficiency virus type 1 is not
a primary determinant of neutralization sensitivity.";
RL J. Virol. 0:0-0(1997).
DR EMBL; AF035533; AAB99954.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
SQ SEQUENCE 857 AA; 97370 MW; 3EB213BD2DCD485D CRC64;

Query Match 100.0%; Score 139; DB 15; Length 857;
Best Local Similarity 100.0%; Pred. No. 1e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCGSKLIC 26
|||||
DB 580 RILAVERYLKDQQLGIWGCGSKLIC 605

RESULT 53

Q71013 PRELIMINARY; PRT; 857 AA.
AC Q71013;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein.
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168C;
RX MEDLINE=95074890; PubMed=7983734;
RA Wrin T., Loh T.P., Vennart J.C., Schuitemaker H., Nunberg J.H.;
RT "Adaptation to persistent growth in the H9 cell line renders a primary
isolate of human immunodeficiency virus type 1 sensitive to
neutralization by vaccine sera.";
RL J. Virol. 69:39-48(1995).
DR EMBL; U15031; AAA64869.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.

Query Match 100.0%; Score 139; DB 15; Length 856;
Best Local Similarity 100.0%; Pred. No. 1e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCGSKLIC 26
|||||
DB 579 RILAVERYLKDQQLGIWGCGSKLIC 604

RESULT 52

O92822 PRELIMINARY; PRT; 857 AA.
AC O92822;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)

DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
SQ SEQUENCE 857 AA; 97505 MW; 039B68247BDC005A CRC64;

Query Match 100.0%; Score 139; DB 15; Length 857;
Best Local Similarity 100.0%; Pred. No. 1e-12; Indels 0; Gaps 0;
Matches 26; Conservative 0; Mismatches 0;

QY 1 RILAVERYLKDQQLGWCSGKLC 26
|||||
Db 580 RILAVERYLKDQQLGWCSGKLC 605

RESULT 54

ID Q89654 PRELIMINARY; PRT; 857 AA.
AC Q89654;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein.
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ACH168.10;
RX MEDLINE=95074890; PubMed=7983734;

RA Wrin T., Loh T.P., Vennari J.C., Schuitemaker H., Nunberg J.H.;
RT "Adaptation to persistent growth in the H9 cell line renders a primary
RT isolate of human immunodeficiency virus type 1 sensitive to
RT neutralization by vaccine sera."
RL J. Virol. 69:39-48(1995).

DR EMBL; U15032; AAA64870.1; -.
DR EMBL; U15030; AAA64868.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Polyprotein;
KW Transmembrane.
SQ SEQUENCE 857 AA; 97361 MW; D4B7A43A0B7E2DB6 CRC64;

Query Match 100.0%; Score 139; DB 15; Length 857;
Best Local Similarity 100.0%; Pred. No. 1e-12; Indels 0; Gaps 0;
Matches 26; Conservative 0; Mismatches 0;

QY 1 RILAVERYLKDQQLGWCSGKLC 26
|||||
Db 580 RILAVERYLKDQQLGWCSGKLC 605

RESULT 55

ID Q92823 PRELIMINARY; PRT; 857 AA.
AC Q92823;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein.
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168C;

RX MEDLINE=95074890; PubMed=7983734;
RA Wrin T., Loh T.P., Vennari J.C., Schuitemaker H., Nunberg J.H.;
RT "Adaptation to persistent growth in the H9 cell line renders a primary
RT isolate of human immunodeficiency virus type 1 sensitive to
RT neutralization by vaccine sera."
RL J. Virol. 69:39-48(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168C;
RA LaCasse R.A., Follis K.E., Moudgil T., Trahey M., Binley J.M.,
RA Planelles V., Zolla-Pazner S., Nunberg J.H.;
RT "Coreceptor utilization by human immunodeficiency virus type 1 is not
RT a primary determinant of neutralization sensitivity."
RL J. Virol. 0:0-0(1997).
DR EMBL; AF035534; RA899955.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
SQ SEQUENCE 857 AA; 97508 MW; D045150ACBDC0BF6 CRC64;

Query Match 100.0%; Score 139; DB 15; Length 857;
Best Local Similarity 100.0%; Pred. No. 1e-12; Indels 0; Gaps 0;
Matches 26; Conservative 0; Mismatches 0;

QY 1 RILAVERYLKDQQLGWCSGKLC 26
|||||
Db 580 RILAVERYLKDQQLGWCSGKLC 605

RESULT 56

Q9QBZ0 PRELIMINARY; PRT; 857 AA.
AC Q9QBZ0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE ENV protein (fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=95CM-MP257;
RX MEDLINE=20122179; PubMed=10659053;
RA Triques K., Bourgeois A., Vidale N., Mpoudi-Ero N., Delaporte E.,
RA Mulanga-Kabeya C., Nzilambi N., Torimiro N., Saman E., Delaporte E.,
RA Peeters M.;
RT "Near-full-length genome sequencing of divergent African HIV type 1
RT subtype F viruses leads to the identification of a new HIV type 1
RT subtype designated K."
RL AIDS Res. Hum. Retroviruses 16:139-151(2000).
DR EMBL; AJ245237; CAB58982.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 1
FT CHAIN 849 857 NEF PROTEIN.
SQ SEQUENCE 857 AA; 97229 MW; 1C81CD10C59379A0 CRC64;

Query Match 100.0%; Score 139; DB 15; Length 857;

Best Local Similarity 100.0%; Pred. No. 1e-12; Mismatches 0; Indels 0; Gaps 0;
Matches 26; Conservative 0;

QY 1 RILAVERYLKDQQLGIWCGSKLIC 26
DB 580 RILAVERYLKDQQLGIWCGSKLIC 605

RESULT 57
Q9YU24 ID Q9YU24 PRELIMINARY; PRT; 859 AA.
AC Q9YU24;
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Envelope glycoprotein.
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]_TaxID=11676;
RP SEQUENCE FROM N.A.
RC STRAIN=SE6594;
RX MEDLINE=99441797; PubMed=10513639;
RA Carr J.K., Laukkanen T., Salminen M.O., Albert J., Alaeus A., Kim B.,
Sanders-Buell E., Birx D.L., McCutchan F.E.;
RT "Characterization of subtype A HIV-1 from Africa by full genome
sequencing.";
RL AIDS 13:1819-1826(1999).
DR EMBL; AF069672; AAD13364.1; -.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0019028; C: viral capsid; IEA.
DR GO; GO:0019031; C: viral envelope; IEA.
DR GO; GO:0005198; F: structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR Pfam; PF00517; GP41; 1.
DR Pfam; PF00516; GP120; 1.
DR InterPro; IPR000777; GP120.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
SQ SEQUENCE 859 AA; 96945 MW; B49458013BA96EB9 CRC64;

Query Match 100.0%; Score 139; DB 15; Length 859;
Best Local Similarity 100.0%; Pred. No. 1e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSKLIC 26
DB 575 RILAVERYLKDQQLGIWCGSKLIC 600

RESULT 58
Q9WLJ1 ID Q9WLJ1 PRELIMINARY; PRT; 859 AA.
AC Q9WLJ1;
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Envelope glycoprotein.
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]_TaxID=11676;
RP SEQUENCE FROM N.A.
RC STRAIN=BFP90;
RX MEDLINE=99039935; PubMed=9824329;
RA Oelrichs R.B., Workman C., Laukkanen T., McCutchan F.E., Deacon N.J.;
RT "A novel subtype A/G/J recombinant full-length HIV type 1 genome from
Burkina Faso.";
RL AIDS Res. Hum. Retroviruses 14:1495-1500(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BFP90;

Oelrichs R.B.;
RA Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF064699; AAD0334.1; -.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0019028; C: viral capsid; IEA.
DR GO; GO:0019031; C: viral envelope; IEA.
DR GO; GO:0005198; F: structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
SQ SEQUENCE 859 AA; 96504 MW; 41BB35F110C38E0C CRC64;

Query Match 100.0%; Score 139; DB 15; Length 859;
Best Local Similarity 100.0%; Pred. No. 1e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSKLIC 26
DB 582 RILAVERYLKDQQLGIWCGSKLIC 607

RESULT 59
Q7SOA7 ID Q7SOA7 PRELIMINARY; PRT; 860 AA.
AC Q7SOA7;
DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Envelope glycoprotein.
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]_TaxID=11676;
RP SEQUENCE FROM N.A.
RC STRAIN=subtype A;
RA Tatsumi M., Matsuda M.;
RT "Infectious DNA clones of HIV-1 subtype A.";
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB098332; BAC77753.1; -.
KW Envelope protein.
SQ SEQUENCE 860 AA; 97452 MW; E694AF763073A6DD CRC64;

Query Match 100.0%; Score 139; DB 15; Length 860;
Best Local Similarity 100.0%; Pred. No. 1e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSKLIC 26
DB 575 RILAVERYLKDQQLGIWCGSKLIC 600

RESULT 60
Q8UNL9 ID Q8UNL9 PRELIMINARY; PRT; 862 AA.
AC Q8UNL9;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Envelope glycoprotein.
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]_TaxID=11676;
RP SEQUENCE FROM N.A.
RC STRAIN=X605;
RA Delgado E., Thomson M.M., Villahermosa M.L., Sierra M., Ocampo A.,
Miralles C., Rodriguez-Perez R., Diz-Aren J., Ojea-de-Castro R.,
Losada E., Cuevas M.T., Vazquez de Parga E., Carmona R.,
Perez Alvarez L., Medrano L., Cuevas L., Taboada J.A., Najera R.;

RT "Identification of a newly characterized HIV-1 BG intersubtype
 RT circulating recombinant form in Galicia, Spain, exhibiting a
 RT pseudotype-like virion structure."
 RL J. Acquir. Immune Defic. Syndr. 0:0-0(2002).
 RN [2]

RP SEQUENCE FROM N.A.
 RC STRAIN=X605;
 RA Delgado E., Thomson M.M., Villahermosa M.L., Sierra M., Ocampo A.,
 RA Miralles C., Rodriguez-Perez R., Diz-Aren J., Ojea-de-Castro R.,
 RA Losada E., Cuevas M.T., Vazquez de Parga E., Carmona R.,
 RA Perez Alvarez L., Medrano L., Cuevas L., Taboada J.A., Najera R.;
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF450096; AL47033.1; -;
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0019028; C:viral capsid; IEA.
 DR GO; GO:0019031; F:structural molecule; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR000328; Env GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
 SQ SEQUENCE 862 AA; 98014 MW; E7AF58E5E93F2B CRC64;

Query Match 100.0%; Score 139; DB 15; Length 862;
 Best Local Similarity 100.0%; Pred. No. 1e-12; Indels 0; Gaps 0;
 Matches 26; Conservative 0; Mismatches 0;

QY 1 RILAVERYLKDQQLGWCSGKLC 26
 |||||
 DB 578 RILAVERYLKDQQLGWCSGKLC 603

RESULT 61

ID Q7SOA2 PRELIMINARY; PRT; 862 AA.
 AC Q7SOA2;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Envelope glycoprotein.
 GN ENV.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=subtype A;
 RA Tatsumi M., Matsuda M.;
 RL "Infectious DNA clones of HIV-1 subtype A."
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB098333; BAC77762.1; -;
 KW Envelope protein.
 SQ SEQUENCE 862 AA; 97469 MW; CB46A4D2982F606E CRC64;

Query Match 100.0%; Score 139; DB 15; Length 862;
 Best Local Similarity 100.0%; Pred. No. 1e-12;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGWCSGKLC 26
 |||||
 DB 577 RILAVERYLKDQQLGWCSGKLC 602

RESULT 62

ID Q9YP39 PRELIMINARY; PRT; 864 AA.
 AC Q9YP39;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Envelope polyprotein.
 GN ENV.

OS Human immunodeficiency virus 1.
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Fang G., Weiser B., Chappey C., Visosky A., Townsend L., Wang Q.,
 RA Burger H.;
 RT "Complete Plasma HIV-1 Sequence: Spl-Promoter Deletion Can Lead to
 RT Non-Progressive Infection."
 RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U69589; AAD10915.1; -;
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0019028; C:viral capsid; IEA.
 DR GO; GO:0019031; F:structural molecule; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR000328; Env GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
 SQ SEQUENCE 864 AA; 98272 MW; C29EE03E9D2D99 CRC64;

Query Match 100.0%; Score 139; DB 15; Length 864;
 Best Local Similarity 100.0%; Pred. No. 1e-12; Indels 0; Gaps 0;
 Matches 26; Conservative 0; Mismatches 0;

QY 1 RILAVERYLKDQQLGWCSGKLC 26
 |||||
 DB 587 RILAVERYLKDQQLGWCSGKLC 612

RESULT 63

ID Q7ZJC8 PRELIMINARY; PRT; 864 AA.
 AC Q7ZJC8;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Envelope glycoprotein.
 GN ENV.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=US4;
 RA Carr J.K., Hierholzer J., Montano S., Hoelscher M., Negrete M.,
 RA Hierholzer M., Avila M., Gomez Carrillo M., Russi J., Vinolas J.,
 RA Alava A., Acosta M., Gianella A., Andrade R., Sanchez J.L.,
 RA Carrion G., Sanchez J., Robb M., Birx D., McCutchan F.;
 RT "Molecular Epidemiology of HIV type 1 in Ecuador, Peru, Bolivia,
 RT Uruguay and Argentina."
 RL AIDS Res. Hum. Retroviruses 0:0-0(2003).
 DR EMBL; AY173955; AAO63221.1; -;
 DR GO; GO:0019031; C:viral envelope; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR000328; Env GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 KW Envelope protein.
 SQ SEQUENCE 864 AA; 97752 MW; 87B26D13FC93552E CRC64;

Query Match 100.0%; Score 139; DB 15; Length 864;
 Best Local Similarity 100.0%; Pred. No. 1e-12; Indels 0; Gaps 0;
 Matches 26; Conservative 0; Mismatches 0;

QY 1 RILAVERYLKDQQLGWCSGKLC 26
 |||||
 DB 587 RILAVERYLKDQQLGWCSGKLC 612

RESULT 64

SQ	SEQUENCE	868 AA; 98621 MW; SEPFEB73B73746FT13 CRC64;
	Query Match	100.0%; Score 139; DB 15; Length 868;
	Best Local Similarity	100.0%; Pred. No. 1e-12;
	Matches	26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1	RILAVERYLKDOQLLGIWGCGSKLIC 26
Db	584	RILAVERYLKDOQLLGIWGCGSKLIC 609
RESULT 66		
Q8Q2X1		
ID	Q8Q2X1	PRELIMINARY; PRT; 870 AA.
AC	Q8Q2X1;	
DT	01-JUN-2002	(TrEMBLrel. 21, Created)
DT	01-JUN-2002	(TrEMBLrel. 21, Last sequence update)
DT	01-JUN-2003	(TrEMBLrel. 24, Last annotation update)
DE	Envelope glycoprotein.	
GN	ENV.	
OS	Human immunodeficiency virus 1.	
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.	
OX	NCBI_TaxID=11676;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RA	Gorry P.R., Taylor J., Holm G., Mehle A., Morgan T., Cayabyab M.,	
RA	Farzan M., Wang H., Bell J.E., Kunstman K.J., Moore J.P.,	
RA	Wolinsky S.M., Gabuzda D.;	
RT	"Increased CCR5 affinity and reduced CCR5/CD4 dependence of a	
RT	neuroinvariant primary human immunodeficiency virus type 1 isolate.";	
RL	J. Virol. 0:0-0(2002).	
DR	EMBL; AF491741; AAM09794.1; -	
DR	GO; GO:0016021; C:integral to membrane; IEA.	
DR	GO; GO:0019028; C:viral capsid; IEA.	
DR	GO; GO:0019031; C:viral envelope; IEA.	
DR	GO; GO:0005198; F:structural molecule activity; IEA.	
DR	InterPro; IPR000328; Env GP41.	
DR	Pfam; PF00516; GP120; 1.	
DR	Pfam; PF00517; GP41; 1.	
KW	AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.	
SQ	SEQUENCE	870 AA; 99067 MW; 067C44F6526160DF CRC64;
	Query Match	100.0%; Score 139; DB 15; Length 870;
	Best Local Similarity	100.0%; Pred. No. 1e-12;
	Matches	26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1	RILAVERYLKDOQLLGIWGCGSKLIC 26
Db	593	RILAVERYLKDOQLLGIWGCGSKLIC 618
RESULT 67		
Q8Q2X0		
ID	Q8Q2X0	PRELIMINARY; PRT; 870 AA.
AC	Q8Q2X0;	
DT	01-JUN-2002	(TrEMBLrel. 21, Created)
DT	01-JUN-2002	(TrEMBLrel. 21, Last sequence update)
DT	01-JUN-2003	(TrEMBLrel. 24, Last annotation update)
DE	Envelope glycoprotein.	
GN	ENV.	
OS	Human immunodeficiency virus 1.	
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.	
OX	NCBI_TaxID=11676;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RA	Gorry P.R., Taylor J., Holm G., Mehle A., Morgan T., Cayabyab M.,	
RA	Farzan M., Wang H., Bell J.E., Kunstman K.J., Moore J.P.,	
RA	Wolinsky S.M., Gabuzda D.;	
RT	"Increased CCR5 affinity and reduced CCR5/CD4 dependence of a	
RT	neuroinvariant primary human immunodeficiency virus type 1 isolate.";	
RL	J. Virol. 0:0-0(2002).	
DR	EMBL; AF491742; AAM09795.1; -	


```
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=96USNG15;
RA Ellenberger D., Sullivan P.S., Dorn J., Schable C., Spira T.J.,
RA Folks T.M., Lal R.B.;
RT "Viral and Immunologic Examination of HIV-1-infected Persistently
RT Seronegative (HIPS) Persons.";
RL J. Infect. Dis. 0:0-0(1999).
DR EMBL; AF157468; AAD45888.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Transmembrane.
FT NON_TER 1
FT NON_TER 117
SQ SEQUENCE 117 AA; 14011 MW; 9A71687C21470B60 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 117;
Best Local Similarity 96.2%; Pred. No. 1.8e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSGKLC 26
|:|||||
Db 19 RVLAVERYLKDQQLGIWCGSGKLC 44

RESULT 72
QYRT2
ID OSYRT2 PRELIMINARY; PRT; 117 AA.
AC OSYRT2;
DT 01-MAY-1999 (TRENBLrel. 10, Created)
DT 01-MAY-1999 (TRENBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=96USNG15;
RA Sullivan P.J., Do A., Ellenberger D.L., Pau C.-P., Paul S., Kalish M.,
RA Robbins K., Lal R., Storck C., Schable C.A., Wise H., Tetteh C.,
RA Jones J., Ward J.;
RT "Surveillance of Central African Nationals living in the United States
RT reveals multiple subtypes of HIV-1 Group M and Group O.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF096334; AAD04409.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Transmembrane.
FT NON_TER 1
FT NON_TER 117
SQ SEQUENCE 117 AA; 13920 MW; 39BD6AAB4FAD37AA CRC64;

Query Match 99.3%; Score 138; DB 15; Length 117;
Best Local Similarity 96.2%; Pred. No. 1.8e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSGKLC 26
|:|||||
Db 19 RVLAVERYLKDQQLGIWCGSGKLC 44

RESULT 73
QYRS4
ID QYRS4 PRELIMINARY; PRT; 117 AA.
AC QYRS4;
DT 01-MAY-1999 (TRENBLrel. 10, Created)
DT 01-MAY-1999 (TRENBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=96USNG46;
RA Sullivan P.J., Do A., Ellenberger D.L., Pau C.-P., Paul S., Kalish M.,
RA Robbins K., Lal R., Storck C., Schable C.A., Wise H., Tetteh C.,
RA Jones J., Ward J.;
RT "Surveillance of Central African Nationals living in the United States
RT reveals multiple subtypes of HIV-1 Group M and Group O.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF096342; AAD04417.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Transmembrane.
FT NON_TER 1
FT NON_TER 117
SQ SEQUENCE 117 AA; 13920 MW; 39BD6AAB4FAD37AA CRC64;

Query Match 99.3%; Score 138; DB 15; Length 117;
Best Local Similarity 96.2%; Pred. No. 1.8e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSGKLC 26
|:|||||
Db 19 RVLAVERYLKDQQLGIWCGSGKLC 44

RESULT 74
QYQNO
ID QYQNO PRELIMINARY; PRT; 117 AA.
AC QYQNO;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Envelope glycoprotein gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=96USHIP89;
RA Ellenberger D., Sullivan P.S., Dorn J., Schable C., Spira T.J.,
RA Folks T.M., Lal R.B.;
RT "Viral and Immunologic Examination of HIV-1-infected Persistently
RT Seronegative (HIPS) Persons.";
RL J. Infect. Dis. 0:0-0(1999).
DR EMBL; AF157473; AAD45893.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Transmembrane.
FT NON_TER 1
FT NON_TER 117
SQ SEQUENCE 117 AA; 13917 MW; E7DBBF9364538256 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 117;
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Best Local Similarity 96.2%; Pred. No. 1.8e-13; Indels 0; Gaps 0;
Matches 25; Conservative 1; Mismatches 0;

QY 1 RILAVERYLKDQQLGIWCSGKLC 26
|:|||||
Db 19 RVLAVERYLKDQQLGIWCSGKLC 44

RESULT 75

Q9YZ04 ID Q9YZ04 PRELIMINARY; PRT; 117 AA.
AC Q9YZ04;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=135.544;
RA Brennan C.A., Lund J.K., Golden A., Yamaguchi J., Vallari A.S.,
RA Phillips J.F., Kacaha P.K., Jackson J.B., Devare S.G.;
RT "serologic and Phylogenetic Characterization of HIV-1 Subtypes in
RT Uganda";
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF006864; AD01308.1; -;
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1 1
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13970 MW; AACAA0502CE79044A CRC64;

Query Match 99.3%; Score 138; DB 15; Length 117;

Best Local Similarity 96.2%; Pred. No. 1.8e-13; Indels 0; Gaps 0;
Matches 25; Conservative 1; Mismatches 0;

QY 1 RILAVERYLKDQQLGIWCSGKLC 26
|:|||||
Db 23 RVLAVERYLKDQQLGIWCSGKLC 48

RESULT 76

Q9YRS6 ID Q9YRS6 PRELIMINARY; PRT; 117 AA.
AC Q9YRS6;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=96USN19;
RA Sullivan P.J., Do A., Ellenberger D.L., Pau C.-P., Paul S., Kalish M.,
RA Robbins K., Lal R., Storck C., Schable C.A., Wise H., Tetteh C.,
RA Jones J., Ward J.;
RT "Surveillance of Central African Nationals living in the United States
RT reveals multiple subtypes of HIV-1 Group M and Group O.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF096340; AD04415.1; -;
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.

DR InterPro; IPR000328; Env_GP41.
KW Transmembrane.
FT NON_TER 1 1
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13864 MW; C8F2F6CBC0A5437P CRC64;

Query Match 99.3%; Score 138; DB 15; Length 117;

Best Local Similarity 96.2%; Pred. No. 1.8e-13; Indels 0; Gaps 0;
Matches 25; Conservative 1; Mismatches 0;

QY 1 RILAVERYLKDQQLGIWCSGKLC 26
|:|||||
Db 19 RVLAVERYLKDQQLGIWCSGKLC 44

RESULT 77

Q9WKU0 ID Q9WKU0 PRELIMINARY; PRT; 117 AA.
AC Q9WKU0;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=96USNG19;
RA Sullivan P.J., Do A., Ellenberger D.L., Pau C.-P., Paul S., Kalish M.,
RA Robbins K., Lal R., Storck C., Schable C.A., Wise H., Tetteh C.,
RA Jones J., Ward J.;
RT "Surveillance of Central African Nationals living in the United States
RT reveals multiple subtypes of HIV-1 Group M and Group O.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF096333; AD04408.1; -;
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1 1
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13959 MW; BBA0CA6FDE179EBC CRC64;

Query Match 99.3%; Score 138; DB 15; Length 117;

Best Local Similarity 96.2%; Pred. No. 1.8e-13; Indels 0; Gaps 0;
Matches 25; Conservative 1; Mismatches 0;

QY 1 RILAVERYLKDQQLGIWCSGKLC 26
|:|||||
Db 19 RVLAVERYLKDQQLGIWCSGKLC 44

RESULT 78

Q9WM72 ID Q9WM72 PRELIMINARY; PRT; 117 AA.
AC Q9WM72;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=140.330;
RA Brennan C.A., Lund J.K., Golden A., Yamaguchi J., Vallari A.S.,

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RA Phillips J.F., Kataaha P.K., Jackson J.B., Devare S.G.;  
RT "Serologic and Phylogenetic Characterization of HIV-1 Subtypes in  
RL Uganda."; [1]  
DR EMBL; AF006868; AAD01312.1; --  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Transmembrane.  
FT NON_TER 1 1  
FT NON_TER 117 117  
SQ SEQUENCE 117 AA; 13954 MW; 423078A5169EB536 CRC64;  
  
Query Match 99.3%; Score 138; DB 15; Length 117;  
Best Local Similarity 96.2%; Pred. No. 1.8e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RILAVERYLKDQQLGIWCGSGKLIIC 26  
Db 23 RVLAVERYLKDQQLGIWCGSGKLIIC 48  
|:|||||||||||||||||  
  
RESULT 79  
ID Q9QON3 PRELIMINARY; PRT; 117 AA.  
AC Q9QON3;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein gp41 (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
OX NCBI_TaxID=11676;  
RN [1]  
RC STRAIN=96USHP82;  
RA Ellenberger D., Sullivan P.S., Dorn J., Schable C., Spira T.J.,  
RA Folks T.M., Lal R.B.;  
RT "Viral and Immunologic Examination of HIV-1-infected Persistently  
RT Seronegative (HPS) Persons."; [1]  
RL J. Infect. Dis. 0:0-0(1999).  
DR EMBL; AF157470; AAD45890.1; --  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Transmembrane.  
FT NON_TER 1 1  
FT NON_TER 117 117  
SQ SEQUENCE 117 AA; 14008 MW; 94D6279CB86297B0 CRC64;  
  
Query Match 99.3%; Score 138; DB 15; Length 117;  
Best Local Similarity 96.2%; Pred. No. 1.8e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RILAVERYLKDQQLGIWCGSGKLIIC 26  
Db 19 RVLAVERYLKDQQLGIWCGSGKLIIC 44  
|:|||||||||||||||||  
  
RESULT 80  
ID Q9YZ01 PRELIMINARY; PRT; 117 AA.  
AC Q9YZ01;  
DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE GP41 (Fragment).  
GN ENV.
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OS Human immunodeficiency virus 1.  
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
OX NCBI_TaxID=11676;  
RN [1]  
RC SEQUENCE FROM N.A.  
RA Brennan C.A., Lund J.K., Golden A., Yamaguchi J., Vallari A.S.,  
RA Phillips J.F., Kataaha P.K., Jackson J.B., Devare S.G.;  
RT "Serologic and Phylogenetic Characterization of HIV-1 Subtypes in  
RT Uganda."; [1]  
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF006872; AAD01316.1; --  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Transmembrane.  
FT NON_TER 1 1  
FT NON_TER 117 117  
SQ SEQUENCE 117 AA; 13950 MW; C3C550C19DB602B6 CRC64;  
  
Query Match 99.3%; Score 138; DB 15; Length 117;  
Best Local Similarity 96.2%; Pred. No. 1.8e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RILAVERYLKDQQLGIWCGSGKLIIC 26  
Db 23 RVLAVERYLKDQQLGIWCGSGKLIIC 48  
|:|||||||||||||||||  
  
RESULT 81  
ID Q9YRS2 PRELIMINARY; PRT; 117 AA.  
AC Q9YRS2;  
DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
OX NCBI_TaxID=11676;  
RN [1]  
RC STRAIN=96USG17;  
RA Sullivan P.J., Do A., Ellenberger D.L., Pau C.-P., Paul S., Kalish M.,  
RA Robbins K., Lal R., Storck C., Schable C.A., Wise H., Tetteh C.,  
RA Jones J., Ward J.;  
RT "Surveillance of Central African Nationals living in the United States  
RT reveals multiple subtypes of HIV-1 Group M and Group O."; [1]  
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF096344; AAD04419.1; --  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Transmembrane.  
FT NON_TER 1 1  
FT NON_TER 117 117  
SQ SEQUENCE 117 AA; 14004 MW; 11CA37F5C8C6278F CRC64;  
  
Query Match 99.3%; Score 138; DB 15; Length 117;  
Best Local Similarity 96.2%; Pred. No. 1.8e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RILAVERYLKDQQLGIWCGSGKLIIC 26  
Db 19 RVLAVERYLKDQQLGIWCGSGKLIIC 44  
|:|||||||||||||||||  
  
RESULT 82
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Q9YZZ2
ID Q9YZZ2 PRELIMINARY; PRT; 117 AA.
AC Q9YZZ2;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=204.987;
RA Brennan C.A., Lund J.K., Golden A., Yamaguchi J., Vallari A.S.,
RA Phillips J.F., Kataaha P.K., Jackson J.B., Devare S.G.;
RT "Serologic and Phylogenetic Characterization of HIV-1 Subtypes in
RT Uganda.";
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF006894; AAD01338.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON TER 1
FT NON TER 117
SQ SEQUENCE 117 AA; 13948 MW; 7FA9BE6B7BF8B39E CRC64;

Query Match 99.3%; Score 138; DB 15; Length 117;
Best Local Similarity 96.2%; Pred. No. 1.8e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGWCSCGKLC 26
Db 23 RVLAVERYLKDQQLGWCSCGKLC 48

RESULT 83
Q7SVI8
ID Q7SVI8 PRELIMINARY; PRT; 117 AA.
AC Q7SVI8;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein gp41 domain (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=99NG681;
RA Zeh C., Agwale S.M., Robbins K.E., Odama L., Sani-Gwarco N.,
RA Gboun M.S., Pieniazek D., Wambele C., Folks T.M., Kalish M.L.;
RT "Presence of HIV-2 subtype B in single and HIV-2 subtype A in dual
RT HIV-1/HIV-2 infections in Nigeria.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY102796; AAM51891.1; -.
KW Envelope protein.
FT NON TER 1
FT NON TER 117
SQ SEQUENCE 117 AA; 14076 MW; F9B2B5A3C415C6F6 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 117;
Best Local Similarity 96.2%; Pred. No. 1.8e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGWCSCGKLC 26
Db 19 RVLAVERYLKDQQLGWCSCGKLC 44

RESULT 84
Q7SVI4
ID Q7SVI4 PRELIMINARY; PRT; 117 AA.
AC Q7SVI4;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein gp41 domain (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=99NG1071;
RA Zeh C., Agwale S.M., Robbins K.E., Odama L., Sani-Gwarco N.,
RA Gboun M.S., Pieniazek D., Wambele C., Folks T.M., Kalish M.L.;
RT "Presence of HIV-2 subtype B in single and HIV-2 subtype A in dual
RT HIV-1/HIV-2 infections in Nigeria.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY102800; AAM51895.1; -.
KW Envelope protein.
FT NON TER 1
FT NON TER 117
SQ SEQUENCE 117 AA; 14009 MW; B4D300DDB4E0A488 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 117;
Best Local Similarity 96.2%; Pred. No. 1.8e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGWCSCGKLC 26
Db 19 RVLAVERYLKDQQLGWCSCGKLC 44

RESULT 85
Q7SVG4
ID Q7SVG4 PRELIMINARY; PRT; 117 AA.
AC Q7SVG4;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein gp41 domain (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=99NG619;
RA Zeh C., Agwale S.M., Robbins K.E., Odama L., Sani-Gwarco N.,
RA Gboun M.S., Pieniazek D., Wambele C., Folks T.M., Kalish M.L.;
RT "Presence of HIV-2 subtype B in single and HIV-2 subtype A in dual
RT HIV-1/HIV-2 infections in Nigeria.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY102820; AAM51915.1; -.
KW Envelope protein.
FT NON TER 1
FT NON TER 117
SQ SEQUENCE 117 AA; 14041 MW; C4195A821EEBB169 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 117;
Best Local Similarity 96.2%; Pred. No. 1.8e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGWCSCGKLC 26
Db 19 RVLAVERYLKDQQLGWCSCGKLC 44

RESULT 86
Q7SVG1
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ID Q7SVG1 PRELIMINARY; PRT; 117 AA.
AC Q7SVG1;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein gp41 domain (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=99NG732;
RA Zeh C., Agwale S.M., Robbins K.E., Odama L., Sani-Gwarco N.,
RA Gboun M.S., Pieniazek D., Wambebe C., Folks T.M., Kalish M.L.;
RT "Presence of HIV-2 subtype B in single and HIV-2 A in dual
RT HIV-1/HIV-2 infections in Nigeria.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY102823; AAM51918.1; -.
KW Envelope protein.
FT NON_TER 1
FT NON_TER 117
SQ SEQUENCE 117 AA; 13960 MW; 9FC5F46458277DDB CRC64;

Query Match 99.3%; Score 138; DB 15; Length 117;
Best Local Similarity 96.2%; Pred. No. 1.8e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCGSKLIC 26
Db 19 RVLAVERYLKDQQLGIWGCGSKLIC 44

RESULT 87
Q7SVF9 PRELIMINARY; PRT; 117 AA.
ID Q7SVF9;
AC Q7SVF9;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein gp41 domain (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=99NG747;
RA Zeh C., Agwale S.M., Robbins K.E., Odama L., Sani-Gwarco N.,
RA Gboun M.S., Pieniazek D., Wambebe C., Folks T.M., Kalish M.L.;
RT "Presence of HIV-2 subtype B in single and HIV-2 A in dual
RT HIV-1/HIV-2 infections in Nigeria.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY102825; AAM51920.1; -.
KW Envelope protein.
FT NON_TER 1
FT NON_TER 117
SQ SEQUENCE 117 AA; 14085 MW; 887D3F6DFEAA6E6 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 117;
Best Local Similarity 96.2%; Pred. No. 1.8e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCGSKLIC 26
Db 19 RVLAVERYLKDQQLGIWGCGSKLIC 44

RESULT 88
Q7SVF7 PRELIMINARY; PRT; 117 AA.
ID Q7SVF7;
AC Q7SVF7;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
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DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein gp41 domain (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=99NG761;
RA Zeh C., Agwale S.M., Robbins K.E., Odama L., Sani-Gwarco N.,
RA Gboun M.S., Pieniazek D., Wambebe C., Folks T.M., Kalish M.L.;
RT "Presence of HIV-2 subtype B in single and HIV-2 A in dual
RT HIV-1/HIV-2 infections in Nigeria.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY102827; AAM51922.1; -.
KW Envelope protein.
FT NON_TER 1
FT NON_TER 117
SQ SEQUENCE 117 AA; 14032 MW; 340A804D7684ADC CRC64;

Query Match 99.3%; Score 138; DB 15; Length 117;
Best Local Similarity 96.2%; Pred. No. 1.8e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCGSKLIC 26
Db 19 RVLAVERYLKDQQLGIWGCGSKLIC 44

RESULT 89
Q7SVF4 PRELIMINARY; PRT; 117 AA.
ID Q7SVF4;
AC Q7SVF4;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein gp41 domain (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=99NG779;
RA Zeh C., Agwale S.M., Robbins K.E., Odama L., Sani-Gwarco N.,
RA Gboun M.S., Pieniazek D., Wambebe C., Folks T.M., Kalish M.L.;
RT "Presence of HIV-2 subtype B in single and HIV-2 A in dual
RT HIV-1/HIV-2 infections in Nigeria.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY102830; AAM51925.1; -.
KW Envelope protein.
FT NON_TER 1
FT NON_TER 117
SQ SEQUENCE 117 AA; 14007 MW; CE92FDEF7CE1E03D CRC64;

Query Match 99.3%; Score 138; DB 15; Length 117;
Best Local Similarity 96.2%; Pred. No. 1.8e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCGSKLIC 26
Db 19 RVLAVERYLKDQQLGIWGCGSKLIC 44

RESULT 90
Q7SVF3 PRELIMINARY; PRT; 117 AA.
ID Q7SVF3;
AC Q7SVF3;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein gp41 domain (Fragment).
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GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
ON NCBI_TaxID=11676;
RX [1]
RC STRAIN=99NG77;
RA Zeh C., Agwale S.M., Robbins K.E., Odama L., Sani-Gwarco N.,
RA Gboun M.S., Pieniazek D., Wambele C., Folks T.M., Kalish M.L.;
RT "Presence of HIV-2 subtype B in single and HIV-2 subtype A in dual
RT HIV-1/HIV-2 infections in Nigeria.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY102831; AM51926.1; -
KW Envelope protein.
FT NON_TER 1
FT NON_TER 117
SQ SEQUENCE 117 AA; 14029 MW; 92B245BDB91467C6 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 117;
Best Local Similarity 96.2%; Pred. No. 1.8e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSGKLC 26
Db 19 RVLAVERYLKDQQLGIWCGSGKLC 44

RESULT 91
Q7SVF2 PRELIMINARY; PRT; 117 AA.
AC Q7SVF2;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Envelope glycoprotein gp41 domain (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RC STRAIN=99NG782;
RA Zeh C., Agwale S.M., Robbins K.E., Odama L., Sani-Gwarco N.,
RA Gboun M.S., Pieniazek D., Wambele C., Folks T.M., Kalish M.L.;
RT "Presence of HIV-2 subtype B in single and HIV-2 subtype A in dual
RT HIV-1/HIV-2 infections in Nigeria.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY102832; AM51927.1; -
KW Envelope protein.
FT NON_TER 1
FT NON_TER 117
SQ SEQUENCE 117 AA; 13937 MW; C30B6DFEDF71B169 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 117;
Best Local Similarity 96.2%; Pred. No. 1.8e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSGKLC 26
Db 19 RVLAVERYLKDQQLGIWCGSGKLC 44

RESULT 92
Q7SVF8 PRELIMINARY; PRT; 117 AA.
AC Q7SVF8;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Envelope glycoprotein gp41 domain (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
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OX NCBI_TaxID=11676;
RN [1]
RC STRAIN=99NG859;
RA Zeh C., Agwale S.M., Robbins K.E., Odama L., Sani-Gwarco N.,
RA Gboun M.S., Pieniazek D., Wambele C., Folks T.M., Kalish M.L.;
RT "Presence of HIV-2 subtype B in single and HIV-2 subtype A in dual
RT HIV-1/HIV-2 infections in Nigeria.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY102836; AM51931.1; -
KW Envelope protein.
FT NON_TER 1
FT NON_TER 117
SQ SEQUENCE 117 AA; 13989 MW; ABA0D93FB50B88E CRC64;

Query Match 99.3%; Score 138; DB 15; Length 117;
Best Local Similarity 96.2%; Pred. No. 1.8e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSGKLC 26
Db 19 RVLAVERYLKDQQLGIWCGSGKLC 44

RESULT 93
Q7SVF7 PRELIMINARY; PRT; 117 AA.
AC Q7SVF7;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Envelope glycoprotein gp41 domain (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RC STRAIN=99NG869;
RA Zeh C., Agwale S.M., Robbins K.E., Odama L., Sani-Gwarco N.,
RA Gboun M.S., Pieniazek D., Wambele C., Folks T.M., Kalish M.L.;
RT "Presence of HIV-2 subtype B in single and HIV-2 subtype A in dual
RT HIV-1/HIV-2 infections in Nigeria.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY102837; AM51932.1; -
KW Envelope protein.
FT NON_TER 1
FT NON_TER 117
SQ SEQUENCE 117 AA; 14076 MW; E3B8E5D24354D5B3 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 117;
Best Local Similarity 96.2%; Pred. No. 1.8e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSGKLC 26
Db 19 RVLAVERYLKDQQLGIWCGSGKLC 44

RESULT 94
Q7SVF4 PRELIMINARY; PRT; 117 AA.
AC Q7SVF4;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Envelope glycoprotein gp41 domain (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RC STRAIN=99NG869;
RA Zeh C., Agwale S.M., Robbins K.E., Odama L., Sani-Gwarco N.,
RA Gboun M.S., Pieniazek D., Wambele C., Folks T.M., Kalish M.L.;
RT "Presence of HIV-2 subtype B in single and HIV-2 subtype A in dual
RT HIV-1/HIV-2 infections in Nigeria.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY102837; AM51932.1; -
KW Envelope protein.
FT NON_TER 1
FT NON_TER 117
SQ SEQUENCE 117 AA; 14076 MW; E3B8E5D24354D5B3 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 117;
Best Local Similarity 96.2%; Pred. No. 1.8e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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RC STRAIN=99NG901;
RA Zen C., Agwale S.M., Robbins K.E., Odama L., Sani-Gwarco M.,
RA Gboun M.S., Pieniazek D., Wambebe C., Folks T.M., Kalish M.L.;
RT "Presence of HIV-2 subtype B in single and HIV-2 subtype A in dual
RT HIV-1/HIV-2 infections in Nigeria.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL; AY102841; AAM51936.1; -.
RW Envelope protein.
KW NON_TER 1
FT NON_TER 117
SQ SEQUENCE 117 AA; 14021 MW; 771766CAD25F3EE4 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 117;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSGKLIC 26
Db 19 RVLAVERYLKDQQLGIWCGSGKLIC 44

RESULT 95
Q95E90 PRELIMINARY; PRT; 118 AA.
AC Q95E90;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CAM19;
RX MEDLINE=20414627; PubMed=10957729;
RA Peter F.N., Eitel M.N., Judith T.N., George A.A., Laura E.T.,
RA John N., Feng G., Mark R., Thomas F.M., Danuta P., Renu L.B.;
RT "Presence of Diverse Human Immunodeficiency Virus Type 1 Viral
RT Variants in Cameroon.";
RL AIDS Res. Hum. Retroviruses 16:1319-1324(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CAM19;
RA Fonjongo P.N., Mpoudi E.N., Torimiro J.N., Alemnji G.A., Eno L.T.,
RA Ngengasong J.N., Gao F., Rayfield M., Folks T.M., Pieniazek D.,
RA Lal R.B.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF252111; AAG14320.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 118
SQ SEQUENCE 118 AA; 14256 MW; CCCA2AF34D192690 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 118;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSGKLIC 26
Db 19 RVLAVERYLKDQQLGIWCGSGKLIC 44

RESULT 96
Q90DJ5 PRELIMINARY; PRT; 121 AA.
AC Q90DJ5;
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DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UG;
RA Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,
RA Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF307736; AAL08797.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 121
SQ SEQUENCE 121 AA; 14560 MW; C4601F79660B8C5D CRC64;

Query Match 99.3%; Score 138; DB 15; Length 121;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSGKLIC 26
Db 19 RVLAVERYLKDQQLGIWCGSGKLIC 44

RESULT 97
Q9EA94 PRELIMINARY; PRT; 122 AA.
AC Q9EA94;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BX513;
RX MEDLINE=20134570; PubMed=10669328;
RA Weidle P.J., Ganea C.E., Irwin K.L., Pieniazek D., McGowan J.P.,
RA Olivo N., Ramos A., Schable C., Lal R.B., Holmberg S.D., Ernst J.A.;
RT "Presence of human immunodeficiency virus (HIV) type 1, group M, non-B
RT subtypes, Bronx, New York: a sentinel site for monitoring HIV genetic
RT diversity in the United States.";
RL Infect. Dis. 181:470-475(2000).
RL EMBL; AF190958; AAG02320.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14674 MW; AFDA96E7701E7E5B CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSGKLIC 26
Db 19 RVLAVERYLKDQQLGIWCGSGKLIC 44
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Db 19 RVLAVERYLKDQQLGIGCSGKLC 44

RESULT 98
Q90DJ2 PRELIMINARY; PRT; 122 AA.
AC Q90DJ2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UG;
RA Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,
RA Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307739; AAL08800.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; F:structural molecule activity; IEA.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1 1
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 14663 MW; AAC57DB097817188 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIGCSGKLC 26
Db 19 RVLAVERYLKDQQLGIGCSGKLC 44

RESULT 99
Q91JUN PRELIMINARY; PRT; 122 AA.
AC Q91JUN;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AR53;
RX MEDLINE=20346416; PubMed=10890362;
RA Masciotra S., Livellara B., Belloso W., Clara L., Tanuri A., Ramos A.,
RA Baggs J., Lal R., Pieniazek D.;
RT "Evidence for a high frequency of HIV-1 subtype F infections among
RT heterosexual population in Buenos Aires, Argentina.";
RL AIDS Res. Hum. Retroviruses 16:1007-1014(2000).
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; F:structural molecule activity; IEA.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1 1
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 14688 MW; 9C80D2BFEAF03B35 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIGCSGKLC 26
Db 19 RVLAVERYLKDQQLGIGCSGKLC 44

RESULT 100
Q9EA85 PRELIMINARY; PRT; 122 AA.
AC Q9EA85;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EX84;
RX MEDLINE=20134570; PubMed=10669328;
RA Weidle P.J., Ganea C.E., Irwin K.L., Pieniazek D., McGowan J.P.,
RA Olivo N., Ramos A., Schable C., Lal R.B., Holmberg S.D., Ernst J.A.;
RT "Presence of human immunodeficiency virus (HIV) type 1, group M, non-B
RT subtypes, Bronx, New York: a sentinel site for monitoring HIV genetic
RT diversity in the United States.";
RL J. Infect. Dis. 181:470-475(2000).
DR EMBL; AF190967; AAG02329.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; F:structural molecule activity; IEA.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1 1
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 14692 MW; F777D665CE19C4E0 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIGCSGKLC 26
Db 19 RVLAVERYLKDQQLGIGCSGKLC 44

RESULT 101
Q9QIW8 PRELIMINARY; PRT; 122 AA.
AC Q9QIW8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GP41ERRJ03;
RA Caride E., Hertogs K., Larder B., Dehertogh P., Brindeiro R.,
RA Machado E., de Sa C.A.M., Eyer W., Passioni L.F.C., Menezes J.A.,
RA Calazans A.R., Tanuri A.;
RT "Genotyping and phenotyping analysis of B and non-B Human
RT immunodeficiency virus type 1 subtypes from patients under HAART.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF165536; AAF08481.1; -.

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DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1 1
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 14708 MW; 4FF31B6E9075EE55 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
|:|||||
Db 19 RVLAVERYLKDQQLGIWGCSGKLIC 44

RESULT 102
Q9QIW1
ID Q9QIW1 PRELIMINARY; PRT; 122 AA.
AC Q9QIW1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GP41ERRJ10;
RA Caride E., Hertogs K., Larder B., Dehertogh P., Brindeiro R.,
RA Machado E., de Sa C.A.M., Eyer W., Passioni L.F.C., Menezes J.A.,
RA Calazans A.R., Tanuri A.;
RT "Genotyping and phenotyping analysis of B and non-B Human
immunodeficiency virus type 1 subtypes from patients under
HAART."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AFI65543; AAF08488.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1 1
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 14733 MW; E2049BD5BAA9A6F0 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
|:|||||
Db 19 RVLAVERYLKDQQLGIWGCSGKLIC 44

RESULT 103
Q9EA81
ID Q9EA81 PRELIMINARY; PRT; 122 AA.
AC Q9EA81;
DT 01-NAR-2001 (TrEMBLrel. 16, Created)
DT 01-NAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=EX923;
RX MEDLINE=20134570; PubMed=10669328;
RA Weidle P.J., Ganea C.E., Irwin K.L., Pieniazek D., McGowan J.P.,
RA Olivo N., Ramos A., Schable C., Lal R.B., Holmberg S.D., Ernst J.A.;
RT "Presence of human immunodeficiency virus (HIV) type 1, group M, non-B
subtypes, Bronx, New York: a sentinel site for monitoring HIV genetic
diversity in the United States."
RL J. Infect. Dis. 181:470-475(2000).
DR EMBL; AF190971; AAG02333.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1 1
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 14753 MW; C3FE4DB1F8B5BCBD CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
|:|||||
Db 19 RVLAVERYLKDQQLGIWGCSGKLIC 44

RESULT 104
Q9YX00
ID Q9YX00 PRELIMINARY; PRT; 122 AA.
AC Q9YX00;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein immunodominant region (fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RJ96BRP043;
RA Tanuri A., Swanson P.A., Devare S.G., Berro O.J., Savedra A.,
RA Costa L.J., Telles J.G., Brindeiro R., Schable C., Pieniazek D.,
RA Rayfield M.;
RT "HIV-1 subtypes among blood donors from Rio de Janeiro, Brazil."
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF034053; AAC79305.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1 1
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 14733 MW; B008FE9FF1F36D0C CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
|:|||||
Db 19 RVLAVERYLKDQQLGIWGCSGKLIC 44

RESULT 105
Q9EAA4
ID Q9EAA4 PRELIMINARY; PRT; 122 AA.
AC Q9EAA4;

DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BX157;
RX MEDLINE=20134570; PubMed=10669328;
RA Weidie P.J., Ganea C.E., Irwin K.L., Pieniazek D., McGowan J.P.,
RA Olivo N., Ramos A., Schable C., Lal R.B., Holmberg S.D., Ernst J.A.;
RT "Presence of human immunodeficiency virus (HIV) type 1, group M, non-B
RT subtypes, Bronx, New York: a sentinel site for monitoring HIV genetic
RT diversity in the United States";
RL J. Infect. Dis. 181:470-475(2000).
RL EMBL; AF190948; AA02310.1; -;
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1 1
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 14805 MW; D9C7A2283538108B CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGWCCKLIC 26
|:|||||
Db 19 RVLAVERYLKDQQLGWCCKLIC 44
|:|||||

RESULT 106
Q9QIWO PRELIMINARY; PRT; 122 AA.
AC Q9QIWO;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GP41ERR11;
RA Carlide E., Hertogs K., Larder B., Dehertogh P., Brindeiro R.,
RA Machado E., de Sa C.A.M., Eyer W., Passioni L.F.C., Menezes J.A.,
RA Calazans A.R., Tanuri A.;
RT "Genotyping and phenotyping analysis of B and non-B Human
RT immunodeficiency virus type 1 subtypes from patients under HAART";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF165544; AA08489.1; -;
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1 1
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 14716 MW; CB39CE85DADE28FE CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGWCCKLIC 26
|:|||||
Db 19 RVLAVERYLKDQQLGWCCKLIC 44
|:|||||

RESULT 107
Q9QDO9 PRELIMINARY; PRT; 122 AA.
AC Q9QDO9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UG;
RA Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,
RA Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;
RT "Similar distribution and continued predominance of HIV-1 subtypes A
RT and D infections in Uganda";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF307672; AAL08733.1; -;
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1 1
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 14684 MW; 52FF3DD5EC29032A CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGWCCKLIC 26
|:|||||
Db 19 RVLAVERYLKDQQLGWCCKLIC 44
|:|||||

RESULT 108
Q9IJUN1 PRELIMINARY; PRT; 122 AA.
AC Q9IJUN1;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AR52;
RX MEDLINE=20346416; PubMed=10890362;
RA Masciotra S., Livellara B., Bellosio W., Clara L., Tanuri A., Ramos A.,
RA Baggs J., Lal R., Pieniazek D.;
RT "Evidence for a high frequency of HIV-1 subtype F infections among
RT heterosexual population in Buenos Aires, Argentina";
RL AIDS Res. Hum. Retroviruses 16:1007-1014(2000).
RL EMBL; AF220701; AAF76820.1; -;
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.

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KW Transmembrane.
FT NON TER 1
FT NON TER 122
SQ SEQUENCE 122 AA; 14917 MW; 69477A001A80725D CRC64;

Query Match
Best Local Similarity 99.3%; Score 138; DB 15; Length 122;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
|:|||||
Db 19 RVLAVERYLKDQQLGIWGCSGKLIC 44

RESULT 109
Q90DK8 PRELIMINARY; PRT; 122 AA.
AC Q90DK8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RC STRAIN=UG;
RA Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,
RA Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;
RT "Similar distribution and continued predominance of HIV-1 subtypes A
RT and D infections in Uganda.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307723; AAL08784.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Transmembrane.
FT NON TER 1
FT NON TER 122
SQ SEQUENCE 122 AA; 14779 MW; 9F2FF45071FB81F9 CRC64;

Query Match
Best Local Similarity 99.3%; Score 138; DB 15; Length 122;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
|:|||||
Db 19 RVLAVERYLKDQQLGIWGCSGKLIC 44

RESULT 110
Q90DS5 PRELIMINARY; PRT; 122 AA.
AC Q90DS5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RC STRAIN=UG;
RA Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,
RA Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;
RT "Similar distribution and continued predominance of HIV-1 subtypes A
RT and D infections in Uganda.";
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RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307656; AAL08717.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Transmembrane.
FT NON TER 1
FT NON TER 122
SQ SEQUENCE 122 AA; 14713 MW; A6117281CEA10231 CRC64;

Query Match
Best Local Similarity 99.3%; Score 138; DB 15; Length 122;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
|:|||||
Db 19 RVLAVERYLKDQQLGIWGCSGKLIC 44

RESULT 111
Q90DQ4 PRELIMINARY; PRT; 122 AA.
AC Q90DQ4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RC STRAIN=UG;
RA Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,
RA Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;
RT "Similar distribution and continued predominance of HIV-1 subtypes A
RT and D infections in Uganda.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307677; AAL08738.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Transmembrane.
FT NON TER 1
FT NON TER 122
SQ SEQUENCE 122 AA; 14678 MW; 4C407CA763CC33F0 CRC64;

Query Match
Best Local Similarity 99.3%; Score 138; DB 15; Length 122;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
|:|||||
Db 19 RVLAVERYLKDQQLGIWGCSGKLIC 44

RESULT 112
Q9EAA5 PRELIMINARY; PRT; 122 AA.
AC Q9EAA5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
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RN  Q9EAA2: PRELIMINARY; PRT; 122 AA.
RP  Q9EAA2;
RC  STRAIN=BX126;
RX  MEDLINE=20134570; PubMed=10669328;
RA  Weidle P.J., Ganea C.E., Irwin K.L., Pieniazek D., McGowan J.P.,
RT  "Presence of human immunodeficiency virus (HIV) type 1, group M, non-B
RT  subtypes, Bronx, New York: a sentinel site for monitoring HIV genetic
RT  diversity in the United States.";
RL  J. Infect. Dis. 181:470-475(2000).
DR  EMBL; AF190947; C:integral to membrane; IEA.
DR  GO; GO:0016021; C:integral to membrane; IEA.
DR  GO; GO:0019031; C:viral envelope; IEA.
DR  GO; GO:0005198; F:structural molecule activity; IEA.
DR  InterPro; IPR000328; Env_GP41.
DR  Pfam; PF00517; GP41; 1.
KW  Transmembrane.
FT  NON_TER 1 1
FT  NON_TER 122 122
SQ  SEQUENCE 122 AA; 14859 MW; E6D2DAD15E71607A CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 R1LAVERYLKDQQLGWCCKLIC 26
DB 19 RVLAVERYLKDQQLGWCCKLIC 44

RESULT 113
Q91JMB PRELIMINARY; PRT; 122 AA.
AC Q91JMB;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RC STRAIN=AR58;
RX MEDLINE=20346416; PubMed=10890362;
RA Masciotra S., Livellara B., Bellosso W., Clara L., Tanuri A., Ramos A.,
RT "Evidence for a high frequency of HIV-1 subtype F infections among
RT heterosexual population in Buenos Aires, Argentina.";
RL AIDS Res. Hum. Retroviruses 16:1007-1014(2000).
DR EMBL; AF220704; AAF76823.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1 1
FT NON_TER 122 122
SQ  SEQUENCE 122 AA; 14735 MW; 040891ADC152BEE4 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 R1LAVERYLKDQQLGWCCKLIC 26
DB 19 RVLAVERYLKDQQLGWCCKLIC 44

RESULT 114
Q9EAA2 PRELIMINARY; PRT; 122 AA.
AC Q9EAA2;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RC STRAIN=UG;
RX Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,
RA Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;
RT "Similar distribution and continued predominance of HIV-1 subtypes A
RT and D infections in Uganda.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307720; AAL08781.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1 1
FT NON_TER 122 122
SQ  SEQUENCE 122 AA; 14603 MW; 0937A2095F3DEFE CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 R1LAVERYLKDQQLGWCCKLIC 26
DB 19 RVLAVERYLKDQQLGWCCKLIC 44
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Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKQQLLGWCGSKGLIC 26
|:|||||
Db 19 RVLAVERYLKQQLLGWCGSKGLIC 44

RESULT 116

Q90DS4
ID Q90DS4 PRELIMINARY; PRT; 122 AA.
AC Q90DS4
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UG;
RA Hu D.J., Bagg J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,
RA Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.,
RT "Similar distribution and continued predominance of HIV-1 subtypes A
RT and D infections in Uganda."
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307657; AAL08718.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR KW Transmembrane.
FT NON_TER 1 1
FT NON_TER 122 122

SEQUENCE 122 AA; 14748 MW; 2BF6CE35DF2E75A3 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;

Best Local Similarity 96.2%; Pred. No. 1.9e-13;

Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKQQLLGWCGSKGLIC 26
|:|||||
Db 19 RVLAVERYLKQQLLGWCGSKGLIC 44

RESULT 117

Q90IW3
ID Q90IW3 PRELIMINARY; PRT; 122 AA.
AC Q90IW3
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GP41ERRJ08;
RA Caride E., Hertogs K., Larder B., Dehertogh P., Brindeiro R.,
RA Machado E., de Sa C.A.M., Eyer W., Passioni L.F.C., Menezes J.A.,
RA Calazans A.R., Tanuri A.;
RT "Genotyping and phenotyping analysis of B and non-B Human
RT immunodeficiency virus type 1 subtypes from patients under HAART."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF165541; AAF08486.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.

Query Match 99.3%; Score 138; DB 15; Length 122;

Best Local Similarity 96.2%; Pred. No. 1.9e-13;

Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKQQLLGWCGSKGLIC 26
|:|||||
Db 19 RVLAVERYLKQQLLGWCGSKGLIC 44

RESULT 118

Q90PX7
ID Q90PX7 PRELIMINARY; PRT; 122 AA.
AC Q90PX7
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TH35;
RA Agwale S.M., Robbins K.E., Odama L., Saekhou A., Zeh C., Edubio A.,
RA Njoku O.M., Sani-Gwarzo N., Gboun M.F., Gao F., Reitz M., Hone D.,
RA Folks T.M., Pieniazek D., Wambebe C., Kalish M.L.;
RT "Development of an env gp41-Based Heteroduplex Mobility Assay for
RT Rapid Human Immunodeficiency Virus Type 1 Subtyping."
RL J. Clin. Microbiol. 39:2110-2114 (2001).
DR EMBL; AF343909; AAK66176.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR KW Transmembrane.
FT NON_TER 1 1
FT NON_TER 122 122

SEQUENCE 122 AA; 14701 MW; 6A9C866990B6F1E CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;

Best Local Similarity 96.2%; Pred. No. 1.9e-13;

Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKQQLLGWCGSKGLIC 26
|:|||||
Db 19 RVLAVERYLKQQLLGWCGSKGLIC 44

RESULT 119

Q9QIV8
ID Q9QIV8 PRELIMINARY; PRT; 122 AA.
AC Q9QIV8
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GP41ERRJ13;
RA Caride E., Hertogs K., Larder B., Dehertogh P., Brindeiro R.,

Query Match 99.3%; Score 138; DB 15; Length 122;

Best Local Similarity 96.2%; Pred. No. 1.9e-13;

Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKQQLLGWCGSKGLIC 26
|:|||||
Db 19 RVLAVERYLKQQLLGWCGSKGLIC 44

RESULT 120

Q9QIV8
ID Q9QIV8 PRELIMINARY; PRT; 122 AA.
AC Q9QIV8
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GP41ERRJ13;
RA Caride E., Hertogs K., Larder B., Dehertogh P., Brindeiro R.,

Query Match 99.3%; Score 138; DB 15; Length 122;

Best Local Similarity 96.2%; Pred. No. 1.9e-13;

Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKQQLLGWCGSKGLIC 26
|:|||||
Db 19 RVLAVERYLKQQLLGWCGSKGLIC 44

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RA Machado E., de Sa C.A.M., Eyer W., Passioni L.F.C., Menezes J.A.,
RA Calazans A.R., Ianuri A.;
RT "Genotyping and phenotyping analysis of B and non-B Human
RT immunodeficiency virus type 1 subtypes from patients under HAART.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF165546; AAF08491.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:vital envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1 1
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 14794 MW; 63071E4A8FB3AB94 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 R1LAVERYLKDQQLGIGWCSGKLC 26
Db 19 RVLAVERYLKDQQLGIGWCSGKLC 44

RESULT 120
Q9WQZ1 ID Q9WQZ1 PRELIMINARY; PRT; 122 AA.
AC Q9WQZ1;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RC STRAIN=TH27;
RA Pieniazek D., Yang C., Lal R.L.;
RT "Phylogenetic analysis of gp41 envelope of HIV-1 groups M, N, and O
RT isolates provides an alternate region for subtype determination.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF113591; AAD42759.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:vital envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1 1
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 14847 MW; 4E202A8C6B404A06 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 R1LAVERYLKDQQLGIGWCSGKLC 26
Db 19 RVLAVERYLKDQQLGIGWCSGKLC 44

RESULT 121
Q90PY1 ID Q90PY1 PRELIMINARY; PRT; 122 AA.
AC Q90PY1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
```

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OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RC STRAIN=97LB10;
RX MEDLINE=21270244; PubMed=11376043;
RA Agwale S.M., Robbins K.E., Odama L., Saekhou A., Zeh C., Eubio A.,
RA Njoku O.M., Sani-Gwarzo N., Gboun M.F., Gao F., Reitz M., Hone D.,
RA Folks T.M., Pieniazek D., Wambebe C., Kalish M.L.;
RT "Development of an env gp41-Based Heteroduplex Mobility Assay for
RT Rapid Human Immunodeficiency Virus Type 1 Subtyping.";
RL J. Clin. Microbiol. 39:2110-2114(2001).
DR EMBL; AF343905; AAK66172.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:vital envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1 1
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 14329 MW; 8D3C10236D47593C CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 R1LAVERYLKDQQLGIGWCSGKLC 26
Db 19 RVLAVERYLKDQQLGIGWCSGKLC 44

RESULT 122
Q9ILL3 ID Q9ILL3 PRELIMINARY; PRT; 122 AA.
AC Q9ILL3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RC STRAIN=UG1994;
RX MEDLINE=20284721; PubMed=10826488;
RA Downing R., Pieniazek D., Hu D.J., Biryahwaho B., Fridlund C.,
RA Rayfield M.A., Sempala S.D., Lal R.B.;
RT "Genetic characterization and phylogenetic analysis of HIV-1 subtype C
RT from Uganda.";
RL AIDS Res. Hum. Retroviruses 16:815-819(2000).
DR EMBL; AF206045; AAF82001.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:vital envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1 1
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 14824 MW; 33645F96145A7B07 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 R1LAVERYLKDQQLGIGWCSGKLC 26
Db 19 R1LAVERYLKDQQLGIGWCSGKLC 44
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RESULT 123
Q90DN6 PRELIMINARY; PRT; 122 AA.
AC Q90DN6;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UG;
RA Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,
RA Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;
RT "Similar distribution and continued predominance of HIV-1 subtypes A
RT and D infections in Uganda.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307695; AAL08756.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Transmembrane.
KW NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14728 MW; EEF439193281EDFE CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLLGWCSGKLIC 26
Db 19 RVLAVERYLKDQQLLGWCSGKLIC 44

RESULT 124
Q90IV7 PRELIMINARY; PRT; 122 AA.
AC Q90IV7;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GP41ERRJ14;
RA Caride E., Hertogs K., Larder B., Dehertogh P., Brindeiro R.,
RA Machado E., de Sa C.A.M., Eyer W., Passioni L.F.C., Menezes J.A.,
RA Calazans A.R., Tanuri A.;
RT "Genotyping and phenotyping analysis of B and non-B Human
RT immunodeficiency virus type 1 subtypes from patients under HAART.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF165547; RAF08492.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Transmembrane.
KW NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14764 MW; 3708166A0368F2A7 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLLGWCSGKLIC 26
Db 19 RVLAVERYLKDQQLLGWCSGKLIC 44

RESULT 125
Q90DP5 PRELIMINARY; PRT; 122 AA.
AC Q90DP5;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UG;
RA Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,
RA Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;
RT "Similar distribution and continued predominance of HIV-1 subtypes A
RT and D infections in Uganda.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307696; AAL08747.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Transmembrane.
KW NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14688 MW; EDA2A13E7C140E32 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLLGWCSGKLIC 26
Db 19 RVLAVERYLKDQQLLGWCSGKLIC 44

RESULT 126
Q90DT0 PRELIMINARY; PRT; 122 AA.
AC Q90DT0;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UG;
RA Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,
RA Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;
RT "Similar distribution and continued predominance of HIV-1 subtypes A
RT and D infections in Uganda.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307651; AAL08712.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
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DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14783 MW; BC2B81D16DEAADF CRC64;

Query Match          99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDOQLLGWCSGKLC 26
   |:|||||
Db 19 RVLAVERYLKDOQLLGWCSGKLC 44
   |:|||||

RESULT 127
Q91JK5 PRELIMINARY; PRT; 122 AA.
AC Q91JK5;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AR49;
RX MEDLINE=20346416; PubMed=10890362;
RA Masciotra S., Livellara B., Bellosso W., Clara L., Tanuri A., Ramos A.,
RA Baggs J., Lal R., Pieniazek D.;
RT "Evidence for a high frequency of HIV-1 subtype F infections among
RT heterosexual population in Buenos Aires, Argentina.";
RL AIDS Res. Hum. Retroviruses 16:1007-1014(2000).
DR EMBL; AF220727; AAF76846.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:001931; C:vital envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14753 MW; 88DF5986C148B527 CRC64;

Query Match          99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDOQLLGWCSGKLC 26
   |:|||||
Db 19 RVLAVERYLKDOQLLGWCSGKLC 44
   |:|||||

RESULT 128
Q9YXN7 PRELIMINARY; PRT; 122 AA.
AC Q9YXN7;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein immunodominant region (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RJ96BRP093;
RA Tanuri A., Swanson P.A., Devare S.G., Berro O.J., Savedra A.,
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RA Costa L.J., Telles J.G., Brindeiro R., Schable C., Pieniazek D.,
RA Rayfield M.;
RT "HIV-1 subtypes among blood donors from Rio de Janeiro, Brazil.";
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF034066; RAC79318.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:001931; C:vital envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14759 MW; 26EB219834EBAE64 CRC64;

Query Match          99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDOQLLGWCSGKLC 26
   |:|||||
Db 19 RVLAVERYLKDOQLLGWCSGKLC 44
   |:|||||

RESULT 129
Q90DP0 PRELIMINARY; PRT; 122 AA.
AC Q90DP0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UG;
RA Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,
RA Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;
RT "Similar distribution and continued predominance of HIV-1 subtypes A
RT and D infections in Uganda.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307691; AAL08752.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:001931; C:vital envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14718 MW; 97207DA63C5007B CRC64;

Query Match          99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDOQLLGWCSGKLC 26
   |:|||||
Db 19 RVLAVERYLKDOQLLGWCSGKLC 44
   |:|||||

RESULT 130
Q9WQZ7 PRELIMINARY; PRT; 122 AA.
AC Q9WQZ7;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
```

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OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=CN37;
RA Pieniazek D., Yang C., Lal R.L.;
RT "Phylogenetic analysis of gp41 envelope of HIV-1 groups M, N, and O
RT isolates provides an alternate region for subtype determination.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF113585; A042753.1; -.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0019031; C:viral envelope; IEA.
DR GO: GO:0005198; F:structural molecule activity; IEA.
DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14807 MW; 7744F5AF97830718 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RILAVERYLKDQQLGIWGCGSKLIC 26
Db 19 RVLAVERYLKDQQLGIWGCGSKLIC 44

RESULT 131
Q90DQ7 PRELIMINARY; PRT; 122 AA.
AC Q90DQ7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=UG;
RA Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,
RA Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;
RT "Similar distribution and continued predominance of HIV-1 subtypes A
RT and D infections in Uganda.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF307674; AAL08735.1; -.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0019031; C:viral envelope; IEA.
DR GO: GO:0005198; F:structural molecule activity; IEA.
DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14740 MW; 33822EBC1A1A3ACE CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RILAVERYLKDQQLGIWGCGSKLIC 26
Db 19 RVLAVERYLKDQQLGIWGCGSKLIC 44

RESULT 132
Q9ILK4 PRELIMINARY; PRT; 122 AA.
ID Q9ILK4
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AC Q9ILK4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=MOZ36;
RX MEDLINE=20284721; PubMed=10826488;
RA Downing R., Pieniazek D., Hu D.J., Biryahwaho B., Fridlund C.,
RA Rayfield M.A., Sempala S.D., Lal R.B.;
RT "Genetic characterization and phylogenetic analysis of HIV-1 subtype C
RT from Uganda.";
RL AIDS Res. Hum. Retroviruses 16:815-819(2000).
DR EMBL: AF206054; AAF82010.1; -.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0019031; C:viral envelope; IEA.
DR GO: GO:0005198; F:structural molecule activity; IEA.
DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14771 MW; BCA91CA7B60ED207 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RILAVERYLKDQQLGIWGCGSKLIC 26
Db 19 RILAVERYLKDQQLGIWGCGSKLIC 44

RESULT 133
Q9YXN4 PRELIMINARY; PRT; 122 AA.
AC Q9YXN4;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein immunodominant region (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=RJ97BRP116;
RA Tanuri A., Swanson P.A., Devare S.G., Berro O.J., Savedra A.,
RA Costa L.J., Telles J.G., Brindeiro R., Schable C., Pieniazek D.,
RA Rayfield M.;
RT "HIV-1 subtypes among blood donors from Rio de Janeiro, Brazil.";
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF034069; AAC79321.1; -.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0019031; C:viral envelope; IEA.
DR GO: GO:0005198; F:structural molecule activity; IEA.
DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14811 MW; F154B211B9D456D5 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY 1 RILAVERYLKDQQLLGWCSGKLC 26
Db 19 RVLAVERYLKDQQLLGWCSGKLC 44

RESULT 134
Q9QIW7 PRELIMINARY; PRT; 122 AA.
AC Q9QIW7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=GP41ERRJ04;
RA Caride E., Hertogs K., Larder B., Dehertogh P., Brindeiro R.,
RA Machado E., de Sa C.A.M., Eyer W., Passioni L.F.C., Menezes J.A.,
RA Calazans A.R., Tanuri A.;
RT "Genotyping and phenotyping analysis of B and non-B Human
RT immunodeficiency virus type 1 subtypes from patients under HAART."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF165537; AAF08482.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1 1
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 14834 MW; 13711994A52A5B33 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLLGWCSGKLC 26
Db 19 RVLAVERYLKDQQLLGWCSGKLC 44

RESULT 135
Q9EA84 PRELIMINARY; PRT; 122 AA.
AC Q9EA84;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=BX88;
RA MEDLINE=20134570; PubMed=10669328;
RA Weidle P.J., Ganea C.E., Irwin K.L., Pieniazek D., McGowan J.P.,
RA Olivo N., Ramos A., Schable C., Lal R.B., Holmberg S.D., Ernst J.A.;
RT "Presence of human immunodeficiency virus (HIV) type 1, group M, non-B
RT subtypes, Bronx, New York: a sentinel site for monitoring HIV genetic
RT diversity in the United States."
RL J. Infect. Dis. 181:470-475 (2000).
DR EMBL; AF190968; AAG02330.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.

QY 1 RILAVERYLKDQQLLGWCSGKLC 26
Db 19 RVLAVERYLKDQQLLGWCSGKLC 44

RESULT 136
Q9IJQ8 PRELIMINARY; PRT; 122 AA.
AC Q9IJQ8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=AR26; PubMed=10890362;
RX MEDLINE=20346416; PubMed=10890362;
RA Masciotra S., Livellara B., Belloso W., Clara L., Tanuri A., Ramos A.,
RA Baggs J., Lal R., Pieniazek D.;
RT "Evidence for a high frequency of HIV-1 subtype F infections among
RT heterosexual population in Buenos Aires, Argentina."
RL AIDS Res. Hum. Retroviruses 16:1007-1014 (2000).
DR EMBL; AF220674; AAF74226.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1 1
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 14733 MW; 89C6303ACD037238 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLLGWCSGKLC 26
Db 19 RVLAVERYLKDQQLLGWCSGKLC 44

RESULT 137
Q9YXR0 PRELIMINARY; PRT; 122 AA.
AC Q9YXR0;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein immunodominant region (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=RJ96BRP025;
RA Tanuri A., Swanson P.A., Devare S.G., Berro O.J., Savendra A.,
RA Costa L.J., Telles J.G., Brindeiro R., Schable C., Pieniazek D.,
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RA Rayfield M.;
 RT "HIV-1 subtypes among blood donors from Rio de Janeiro, Brazil.";
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF034043; AAC79295.1; -;
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0019031; C:viral envelope; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR000328; Env_GP41.
 DR Pfam; PF00517; GP41; 1.
 KW Transmembrane.
 FT NON_TER 1 1
 FT NON_TER 122 122
 SQ SEQUENCE 122 AA; 14795 MW; 313ED9A97E83167C CRC64;
 Query Match 99.3%; Score 138; DB 15; Length 122;
 Best Local Similarity 96.2%; Pred. No. 1.9e-13;
 Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RILAVERYLKDQQLGIWCGSGKLC 26
 Db 19 RVLAVERYLKDQQLGIWCGSGKLC 44
 RESULT 138
 ID Q90DN0 PRELIMINARY; PRT; 122 AA.
 AC Q90DN0;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Envelope glycoprotein (Fragment).
 GN ENV.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OC NCBI_TaxID=11676;
 RN [1]
 RC STRAIN=UG;
 RA Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C., Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Ial R.;
 RT "Similar distribution and continued predominance of HIV-1 subtypes A and D infections in Uganda.";
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF307701; AAL08762.1; -;
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0019031; C:viral envelope; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR000328; Env_GP41.
 DR Pfam; PF00517; GP41; 1.
 KW Transmembrane.
 FT NON_TER 1 1
 FT NON_TER 122 122
 SQ SEQUENCE 122 AA; 14712 MW; 960D670EAF51F06 CRC64;
 Query Match 99.3%; Score 138; DB 15; Length 122;
 Best Local Similarity 96.2%; Pred. No. 1.9e-13;
 Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RILAVERYLKDQQLGIWCGSGKLC 26
 Db 19 RVLAVERYLKDQQLGIWCGSGKLC 44
 RESULT 139
 ID Q9YXQ7 PRELIMINARY; PRT; 122 AA.
 AC Q9YXQ7;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Envelope glycoprotein immunodominant region (Fragment).
 GN ENV.
 OS Human immunodeficiency virus 1.

OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OC NCBI_TaxID=11676;
 RN [1]
 RC SEQUENCE FROM N.A.
 RA Tanuri A., Swanson P.A., Devare S.G., Berro O.J., Savedra A., Costa L.J., Telles J.G., Brindeiro R., Schable C., Pieniazek D., Rayfield M.;
 RT "HIV-1 subtypes among blood donors from Rio de Janeiro, Brazil.";
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF034046; AAC79298.1; -;
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0019031; C:viral envelope; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR000328; Env_GP41.
 DR Pfam; PF00517; GP41; 1.
 KW Transmembrane.
 FT NON_TER 1 1
 FT NON_TER 122 122
 SQ SEQUENCE 122 AA; 14635 MW; 906927994C59310A CRC64;
 Query Match 99.3%; Score 138; DB 15; Length 122;
 Best Local Similarity 96.2%; Pred. No. 1.9e-13;
 Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RILAVERYLKDQQLGIWCGSGKLC 26
 Db 19 RVLAVERYLKDQQLGIWCGSGKLC 44
 RESULT 140
 ID Q9YXP9 PRELIMINARY; PRT; 122 AA.
 AC Q9YXP9;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Envelope glycoprotein immunodominant region (Fragment).
 GN ENV.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OC NCBI_TaxID=11676;
 RN [1]
 RC SEQUENCE FROM N.A.
 RA Tanuri A., Swanson P.A., Devare S.G., Berro O.J., Savedra A., Costa L.J., Telles J.G., Brindeiro R., Schable C., Pieniazek D., Rayfield M.;
 RT "HIV-1 subtypes among blood donors from Rio de Janeiro, Brazil.";
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF034054; AAC79306.1; -;
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0019031; C:viral envelope; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR000328; Env_GP41.
 DR Pfam; PF00517; GP41; 1.
 KW Transmembrane.
 FT NON_TER 1 1
 FT NON_TER 122 122
 SQ SEQUENCE 122 AA; 14678 MW; A7C3DAFC2CE00A3D CRC64;
 Query Match 99.3%; Score 138; DB 15; Length 122;
 Best Local Similarity 96.2%; Pred. No. 1.9e-13;
 Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RILAVERYLKDQQLGIWCGSGKLC 26
 Db 19 RVLAVERYLKDQQLGIWCGSGKLC 44
 RESULT 141
 ID Q90DI9 PRELIMINARY; PRT; 122 AA.


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AC Q90DI9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UG;
RA Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,
RA Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;
RA Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF307742; AAL08803.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1 1
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 14717 MW; 399CE05F0C36976 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGICSGKLC 26
Db 19 RVLAVERYLKDQQLGICSGKLC 44

RESULT 142
Q90DN2
ID Q90DN2 PRELIMINARY; PRT; 122 AA.
AC Q90DN2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UG;
RA Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,
RA Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;
RA "Similar distribution and continued predominance of HIV-1 subtypes A
RT and D infections in Uganda.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307699; AAL08760.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1 1
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 14684 MW; 71EA72685F2915C3 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGICSGKLC 26
Db 19 RVLAVERYLKDQQLGICSGKLC 44

RESULT 143
Q9YXR4
ID Q9YXR4 PRELIMINARY; PRT; 122 AA.
AC Q9YXR4;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein immunodominant region (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RJ96BR009;
RA Tanuri A., Swanson P.A., Devare S.G., Berro O.J., Savedra A.,
RA Costa L.J., Telles J.G., Brindeiro R., Schable C., Pieniazek D.,
RA Rayfield M.;
RT "HIV-1 subtypes among blood donors from Rio de Janeiro, Brazil.";
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF034039; AAC79291.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1 1
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 14739 MW; 40D4789EB8C888C2 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGICSGKLC 26
Db 19 RVLAVERYLKDQQLGICSGKLC 44

RESULT 144
Q9IJQ7
ID Q9IJQ7 PRELIMINARY; PRT; 122 AA.
AC Q9IJQ7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AR32;
RX MEDLINE=20346416; PubMed=10890362;
RA Masciora S., Livellara B., Bellosso W., Clara L., Tanuri A., Ramos A.,
RA Baggs J., Lal R., Pieniazek D.;
RT "Evidence for a high frequency of HIV-1 subtype F infections among
RT heterosexual population in Buenos Aires, Argentina.";
RL AIDS Res. Hum. Retroviruses 16:1007-1014(2000).
DR EMBL; AF220675; AAF74227.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1 1
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 14778 MW; DC8AE743D5815680 CRC64;
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Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSGKLC 26
|:|||||
Db 19 RVLAVERYLKDQQLGIWCGSGKLC 44

RESULT 145

Q9IUL2 PRELIMINARY; PRT; 122 AA.
AC Q9IUL2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=AR44;
RX MEDLINE=20346416; PubMed=10890362;
RA Masciotra S., Livellara B., Belluso W., Clara L., Tanuri A., Ramos A.,
RA Baggs J., Lal R., Pieniazek D.;
RT "Evidence for a high frequency of HIV-1 subtype F infections among
RT heterosexual population in Buenos Aires, Argentina.";
RL AIDS Res. Hum. Retroviruses 16:1007-1014(2000).
DR EMBL; AF220720; AAF76839.1; -;
GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1 1
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 14755 MW; 0D30DB46BF54A8FA CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSGKLC 26
|:|||||
Db 19 RVLAVERYLKDQQLGIWCGSGKLC 44

RESULT 146

Q9ODR7 PRELIMINARY; PRT; 122 AA.
AC Q9ODR7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=UG;
RA Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,
RA Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;
RT "Similar distribution and continued predominance of HIV-1 subtypes A
RT and D infections in Uganda.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307664; AAL08725.1; -;
GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1 1
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 14693 MW; D20269AD4ADF8DEE CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSGKLC 26
|:|||||
Db 19 RVLAVERYLKDQQLGIWCGSGKLC 44

RESULT 147

Q9ODR8 PRELIMINARY; PRT; 122 AA.
AC Q9ODR8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=UG;
RA Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,
RA Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;
RT "Similar distribution and continued predominance of HIV-1 subtypes A
RT and D infections in Uganda.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307663; AAL08724.1; -;
GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1 1
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 14719 MW; 2DDC88C8BD61B23B0 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSGKLC 26
|:|||||
Db 19 RVLAVERYLKDQQLGIWCGSGKLC 44

RESULT 148

Q9YXQ1 PRELIMINARY; PRT; 122 AA.
AC Q9YXQ1;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein immunodominant region (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=RJ96ERP042;

```
RA Tanuri A., Swanson P.A., Devare S.G., Berro O.J., Savedra A.,
RA Costa L.J., Telles J.G., Brindeiro R., Schable C., Pieniazek D.,
RA Rayfield M.;
RT "HIV-1 subtypes among blood donors from Rio de Janeiro, Brazil.";
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR ENBL; AF034052; AAC79304.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14792 MW; 7D5BB601468FD17 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLLGWCGSKGLIC 26
|:|||||
Db 19 RVLAVERYLKDQQLLGWCGSKGLIC 44

RESULT 149
Q90DN9 PRELIMINARY; PRT; 122 AA.
AC Q90DN9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RC STRAIN=UG;
RA Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,
RA Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondoro T.J., Lal R.;
RT "Similar distribution and continued predominance of HIV-1 subtypes A
RT and D infections in Uganda.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR ENBL; AF307692; AAL08753.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14814 MW; 151A3B6C2ED545E9 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLLGWCGSKGLIC 26
|:|||||
Db 19 RVLAVERYLKDQQLLGWCGSKGLIC 44

RESULT 150
Q9QIV3 PRELIMINARY; PRT; 122 AA.
AC Q9QIV3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RC STRAIN=UG;
RA Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,
RA Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondoro T.J., Lal R.;
RT "Similar distribution and continued predominance of HIV-1 subtypes A
RT and D infections in Uganda.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR ENBL; AF307692; AAL08753.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14814 MW; 151A3B6C2ED545E9 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLLGWCGSKGLIC 26
|:|||||
Db 19 RVLAVERYLKDQQLLGWCGSKGLIC 44

RESULT 151
Q9IUL3 PRELIMINARY; PRT; 122 AA.
AC Q9IUL3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RC STRAIN=AR43;
RX MEDLINE=20346416; PubMed=10890362;
RA Baggiotta S., Livellara B., Bellosso W., Clara L., Tanuri A., Ramos A.,
RA Baggs J., Lal R., Pieniazek D.;
RT "Evidence for a high frequency of HIV-1 subtype F infections among
RT heterosexual population in Buenos Aires, Argentina.";
RL AIDS Res. Hum. Retroviruses 16:1007-1014 (2000).
DR ENBL; AF220719; AAF76838.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14768 MW; 081673FD2DDA42D3 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLLGWCGSKGLIC 26
|:|||||
Db 19 RVLAVERYLKDQQLLGWCGSKGLIC 44
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GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN=GP41ERRJ18;
RA Caride E., Hertogs K., Larder B., Dehertogh P., Brindeiro R.,
RA Machado E., de Sa C.A.M., Eyer W., Passioni L.F.C., Menezes J.A.,
RA Calazans A.R., Tanuri A.;
RT "Genotyping and phenotyping analysis of B and non-B Human
RT immunodeficiency virus type 1 subtypes from patients under HAART.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR ENBL; AF165551; AAF08496.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14644 MW; FEB52F3423DCC29F CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLLGWCGSKGLIC 26
|:|||||
Db 19 RVLAVERYLKDQQLLGWCGSKGLIC 44

RESULT 151
Q9IUL3 PRELIMINARY; PRT; 122 AA.
AC Q9IUL3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN=AR43;
RX MEDLINE=20346416; PubMed=10890362;
RA Baggiotta S., Livellara B., Bellosso W., Clara L., Tanuri A., Ramos A.,
RA Baggs J., Lal R., Pieniazek D.;
RT "Evidence for a high frequency of HIV-1 subtype F infections among
RT heterosexual population in Buenos Aires, Argentina.";
RL AIDS Res. Hum. Retroviruses 16:1007-1014 (2000).
DR ENBL; AF220719; AAF76838.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14768 MW; 081673FD2DDA42D3 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLLGWCGSKGLIC 26
|:|||||
Db 19 RVLAVERYLKDQQLLGWCGSKGLIC 44
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RESULT 152
Q9EA95
ID Q9EA95 PRELIMINARY; PRT; 122 AA.
AC Q9EA95;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BX435;
RX MEDLINE=20134570; PubMed=10669328;
RA Weidle P.J., Ganea C.E., Irwin K.L., Pieniazek D., McGowan J.P.,
RA Olivo N., Ramos A., Schable C., Lal R.B., Holmberg S.D., Ernst J.A.;
RT "Presence of human immunodeficiency virus (HIV) type 1, group M, non-B
RT subtypes, Bronx, New York: a sentinel site for monitoring HIV genetic
RT diversity in the United States.";
RL J. Infect. Dis. 181:470-475(2000).
DR ENBL; AF190957; AG02319.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Transmembrane.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
FT NON_TER 122
SQ SEQUENCE 122 AA; 14767 MW; 363549B0844EDEE5 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCSGKLC 26
|:|||||
Db 19 RVLAVERYLKDQQLGIWCSGKLC 44
|:|||||

RESULT 153
Q9ODL7
ID Q9ODL7 PRELIMINARY; PRT; 122 AA.
AC Q9ODL7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UG;
RA Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,
RA Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;
RT "Similar distribution and continued predominance of HIV-1 subtypes A
RT and D infections in Uganda.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR ENBL; AF307740; AAL08801.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Transmembrane.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
FT NON_TER 122
SQ SEQUENCE 122 AA; 14693 MW; ED14B39C32BE0986 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCSGKLC 26
|:|||||
Db 19 RVLAVERYLKDQQLGIWCSGKLC 44
|:|||||

RESULT 154
Q9ODQ8
ID Q9ODQ8 PRELIMINARY; PRT; 122 AA.
AC Q9ODQ8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UG;
RA Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,
RA Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;
RT "Similar distribution and continued predominance of HIV-1 subtypes A
RT and D infections in Uganda.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR ENBL; AF307740; AAL08801.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Transmembrane.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
FT NON_TER 122
SQ SEQUENCE 122 AA; 14693 MW; ED14B39C32BE0986 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCSGKLC 26
|:|||||
Db 19 RVLAVERYLKDQQLGIWCSGKLC 44
|:|||||

RESULT 155
Q9ODJ1
ID Q9ODJ1 PRELIMINARY; PRT; 122 AA.
AC Q9ODJ1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UG;
RA Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,
RA Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;
RT "Similar distribution and continued predominance of HIV-1 subtypes A
RT and D infections in Uganda.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR ENBL; AF307740; AAL08801.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Transmembrane.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
FT NON_TER 122
SQ SEQUENCE 122 AA; 14712 MW; 34B609D400C67CC5 CRC64;
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DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14816 MW; 6BD0DF2301B4043A CRC64;

Query Match          99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLC 26
Db 19 RVLAVERYLKDQQLGIWGCSGKLC 44

RESULT 156
Q9YXM8 PRELIMINARY; PRT; 122 AA.
AC Q9YXM8;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Envelope glycoprotein immunodominant region (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrov. viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RJ97BRP132;
RA Tanuri A., Swanson P.A., Devare S.G., Berro O.J., Savedra A.,
RA Costa L.J., Telles J.G., Brindeiro R., Schable C., Pieniazek D.,
RA Rayfield M.;
RT "HIV-1 subtypes among blood donors from Rio de Janeiro, Brazil.";
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF034075; AAC79327.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14571 MW; A5E7A49C0F1BA3AF CRC64;

Query Match          99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLC 26
Db 19 RVLAVERYLKDQQLGIWGCSGKLC 44

RESULT 157
Q90DI8 PRELIMINARY; PRT; 122 AA.
AC Q90DI8;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrov. viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UG;
RA Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,
RA Biryahwahwo B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF307743; AAL08804.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14664 MW; 637EF68FDDC36A11 CRC64;

Query Match          99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLC 26
Db 19 RVLAVERYLKDQQLGIWGCSGKLC 44

RESULT 158
Q9IJN7 PRELIMINARY; PRT; 122 AA.
AC Q9IJN7;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrov. viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AR33;
RA MEDLINE=20346416; PubMed=10890362;
RA Masciotra S., Livellara B., Belloso W., Clara L., Tanuri A., Ramos A.,
RA Baggs J., Lal R., Pieniazek D.;
RT "Evidence for a high frequency of HIV-1 subtype F infections among
RT heterosexual population in Buenos Aires, Argentina.";
RL AIDS Res. Hum. Retroviruses 16:1007-1014(2000).
DR EMBL; AF220695; AAF76814.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14704 MW; FDF3BD3C77B74A23 CRC64;

Query Match          99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLC 26
Db 19 RVLAVERYLKDQQLGIWGCSGKLC 44

RESULT 159
Q90DS6 PRELIMINARY; PRT; 122 AA.
AC Q90DS6;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrov. viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
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RN RP SEQUENCE FROM N.A.
RC STRAIN=UG;
RA Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,
RA Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;
RT "Similar distribution and continued predominance of HIV-1 subtypes A
RT and D infections in Uganda.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307655; AAL08716.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14703 MW; 78DBC3BD63CE0776 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSGKLC 26
Db 19 RVLAVERYLKDQQLGIWCGSGKLC 44

RESULT 160
Q90DP3 ID Q90DP3 PRELIMINARY; PRT; 122 AA.
AC Q90DP3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN RP SEQUENCE FROM N.A.
RC STRAIN=UG;
RA Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,
RA Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;
RT "Similar distribution and continued predominance of HIV-1 subtypes A
RT and D infections in Uganda.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307688; AAL08749.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14818 MW; ACS5D1B6C79749B83 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSGKLC 26
Db 19 RVLAVERYLKDQQLGIWCGSGKLC 44

RESULT 161
Q90DK0 ID Q90DK0 PRELIMINARY; PRT; 122 AA.
AC Q90DK0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
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DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN RP SEQUENCE FROM N.A.
RC STRAIN=UG;
RA Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,
RA Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;
RT "Similar distribution and continued predominance of HIV-1 subtypes A
RT and D infections in Uganda.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307731; AAL08792.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14742 MW; D4BE2130CDC37338 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSGKLC 26
Db 19 RVLAVERYLKDQQLGIWCGSGKLC 44

RESULT 162
Q90DR3 ID Q90DR3 PRELIMINARY; PRT; 122 AA.
AC Q90DR3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN RP SEQUENCE FROM N.A.
RC STRAIN=UG;
RA Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,
RA Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;
RT "Similar distribution and continued predominance of HIV-1 subtypes A
RT and D infections in Uganda.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307668; AAL08729.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14704 MW; FA86E5277AD367DC CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSGKLC 26
Db 19 RVLAVERYLKDQQLGIWCGSGKLC 44
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RESULT 163
ID Q91JN6 PRELIMINARY; PRT; 122 AA.
AC Q91JN6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RC STRAIN=AR34;
RX MEDLINE=20346416; PubMed=10890362;
RA Masciotra S., Livellara B., Belioso W., Clara L., Tanuri A., Ramos A.,
RA Baggs J., Lal R., Pieniazek D.;
RT "Evidence for a high frequency of HIV-1 subtype F infections among
RT heterosexual population in Buenos Aires, Argentina.";
RL AIDS Res. Hum. Retroviruses 16:1007-1014(2000).
DR EMBL, AF220696; AAF76815.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14718 MW; E822C25F0AAE61F1 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 R1LAVERYLKDQQLGIWCSGKLC 26
|:|||||
Db 19 RVLAVERYLKDQQLGIWCSGKLC 44

RESULT 164
ID Q90DR2 PRELIMINARY; PRT; 122 AA.
AC Q90DR2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RC STRAIN=UG;
RA Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,
RA Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;
RT "Similar distribution and continued predominance of HIV-1 subtypes A
RT and D infections in Uganda.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307683; AAL08744.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14703 MW; 26D08CB693C40653 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 R1LAVERYLKDQQLGIWCSGKLC 26
|:|||||
Db 19 RVLAVERYLKDQQLGIWCSGKLC 44

RESULT 165
ID Q90DP8 PRELIMINARY; PRT; 122 AA.
AC Q90DP8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RC STRAIN=UG;
RA Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,
RA Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;
RT "Similar distribution and continued predominance of HIV-1 subtypes A
RT and D infections in Uganda.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307683; AAL08744.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14703 MW; 26D08CB693C40653 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 R1LAVERYLKDQQLGIWCSGKLC 26
|:|||||
Db 19 RVLAVERYLKDQQLGIWCSGKLC 44

RESULT 166
ID Q91LJ6 PRELIMINARY; PRT; 122 AA.
AC Q91LJ6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RC STRAIN=ZIM29;
RX MEDLINE=20284721; PubMed=10826488;
RA Downing R., Pieniazek D., Hu D.J., Biryahwaho B., Fridlund C.,
RA Rayfield M.A., Sempala S.D., Lal R.B.;
RT "Genetic characterization and phylogenetic analysis of HIV-1 subtype C
RT from Uganda.";
RL AIDS Res. Hum. Retroviruses 16:815-819(2000).
DR EMBL; AF206062; AAF82018.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
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DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14746 MW; 194509B404DDDC61B CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLC 26
|:|||||
Db 19 RVLAVERYLKDQQLGIWGCSGKLC 44

RESULT 167

Q9IJP6 PRELIMINARY; PRT; 122 AA.
AC Q9IJP6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AR15;
RX MEDLINE=20346416; PubMed=10890362;
RA Masciotra S., Livellara B., Bellosso W., Clara L., Tanuri A., Ramos A.,
RA Bagges J., Lal R., Pieniazek D.;
RT "Evidence for a high frequency of HIV-1 subtype F infections among
RT heterosexual population in Buenos Aires, Argentina.";
RL AIDS Res. Hum. Retroviruses 16:1007-1014 (2000).
DR EMBL; AF220686; AAF74238.1; -;
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14729 MW; D1CF7E2498427841 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLC 26
|:|||||
Db 19 RVLAVERYLKDQQLGIWGCSGKLC 44

RESULT 168

Q9EA88 PRELIMINARY; PRT; 122 AA.
AC Q9EA88;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=BX797;
RX MEDLINE=20134570; PubMed=10669328;
RA Weidle P.J., Ganea C.E., Irwin K.L., Pieniazek D., McGowan J.P.,
RA Olivo N., Ramos A., Schable C., Lal R.B., Holmberg S.D., Ernst J.A.;
RT "Presence of human immunodeficiency virus (HIV) type 1, group M, non-B
RT subtypes, Bronx, New York: a sentinel site for monitoring HIV genetic
RT diversity in the United States.";
RL J. Infect. Dis. 181:470-475 (2000).
DR EMBL; AF190964; AAG02326.1; -;
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14661 MW; 11024C717439B83A CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLC 26
|:|||||
Db 19 RVLAVERYLKDQQLGIWGCSGKLC 44

RESULT 169

Q90DS1 PRELIMINARY; PRT; 122 AA.
AC Q90DS1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UG;
RA Hu D.J., Bagges J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,
RA Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;
RT "Similar distribution and continued predominance of HIV-1 subtypes A
RT and D infections in Uganda.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307660; AAL08721.1; -;
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14727 MW; 63657CA763C369EF CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLC 26
|:|||||
Db 19 RVLAVERYLKDQQLGIWGCSGKLC 44

RESULT 170

Q9IJ06 PRELIMINARY; PRT; 122 AA.
AC Q9IJ06;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)

[illegible]

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SQ SEQUENCE 122 AA; 14684 MW; AEBB7D3AE1B0BE23 CRC64;
Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
|:|||||
19 RVLAVERYLKDQQLGIWGCSGKLIC 44

RESULT 174
Q90DM2 PRELIMINARY; PRT; 122 AA.
AC Q90DM2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
[1]
RN STRAIN=UG;
RA Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,
Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;
RT "Similar distribution and continued predominance of HIV-1 subtypes A
and D infections in Uganda."
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307709; AAL08770.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
FT NON_TER 122
SQ SEQUENCE 122 AA; 14797 MW; 70078BACAF37931 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
|:|||||
19 RVLAVERYLKDQQLGIWGCSGKLIC 44

RESULT 175
Q90DN3 PRELIMINARY; PRT; 122 AA.
AC Q90DN3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
[1]
RN STRAIN=UG;
RA Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,
Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;
RT "Similar distribution and continued predominance of HIV-1 subtypes A
and D infections in Uganda."
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307698; AAL08759.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
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DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
FT NON_TER 122
SQ SEQUENCE 122 AA; 14848 MW; FEF3F75550D01A63 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
|:|||||
19 RVLAVERYLKDQQLGIWGCSGKLIC 44

RESULT 176
Q91JP2 PRELIMINARY; PRT; 122 AA.
AC Q91JP2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
[1]
RN STRAIN=AR22;
RA MEDLINE=20346416; PubMed=10890362;
RX Masciotra S., Livellara B., Belloso W., Clara L., Tanuri A.,
Baggs J., Lal R., Pieniazek D.;
RT "Evidence for a high frequency of HIV-1 subtype F infections among
heterosexual population in Buenos Aires, Argentina."
RL AIDS Res. Hum. Retroviruses 16:1007-1014(2000).
DR EMBL; AF220690; AAF76809.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
FT NON_TER 122
SQ SEQUENCE 122 AA; 14748 MW; 61E64BBC3F42460A CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
|:|||||
19 RVLAVERYLKDQQLGIWGCSGKLIC 44

RESULT 177
Q90DS7 PRELIMINARY; PRT; 122 AA.
AC Q90DS7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
[1]
RN STRAIN=FROM N.A.
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RC STRAIN=UC;
RA Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,
RA Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;
RT "Similar distribution and continued predominance of HIV-1 subtypes A
RT and D infections in Uganda.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR ENBL; AF307654; AL08715.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Transmembrane.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
FT NON_TER 122
SQ SEQUENCE 122 AA; 14861 MW; CE141B85AF77D68C CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 R1LAVERYLKDQQLGIWCSGKLC 26
Db 19 RVLAVERYLKDQQLGIWCSGKLC 44

RESULT 178
ID Q9QIU7 PRELIMINARY; PRT; 122 AA.
AC Q9QIU7
RC STRAIN=GP41ERRJ24;
RA Caride E., Hertoghs K., Larder B., Dehertogh P., Brindeiro R.,
RA Machado E., de Sa C.A.M., Eyer W., Passioni L.F.C., Menezes J.A.,
RA Calazans A.R., Tanuri A.;
RT "Genotyping and phenotyping analysis of B and non-B Human
RT immunodeficiency virus type 1 subtypes from patients under HAART.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR ENBL; AF165557; AAF08502.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Transmembrane.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
FT NON_TER 122
SQ SEQUENCE 122 AA; 14635 MW; D052E4B73AE3008E CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 R1LAVERYLKDQQLGIWCSGKLC 26
Db 19 RVLAVERYLKDQQLGIWCSGKLC 44

RESULT 179
ID Q9IJQ1 PRELIMINARY; PRT; 122 AA.
AC Q9IJQ1
RC STRAIN=GP41ERRJ24;
RA Caride E., Hertoghs K., Larder B., Dehertogh P., Brindeiro R.,
RA Machado E., de Sa C.A.M., Eyer W., Passioni L.F.C., Menezes J.A.,
RA Calazans A.R., Tanuri A.;
RT "Genotyping and phenotyping analysis of B and non-B Human
RT immunodeficiency virus type 1 subtypes from patients under HAART.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR ENBL; AF165557; AAF08502.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Transmembrane.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
FT NON_TER 122
SQ SEQUENCE 122 AA; 14635 MW; D052E4B73AE3008E CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 R1LAVERYLKDQQLGIWCSGKLC 26
Db 19 RVLAVERYLKDQQLGIWCSGKLC 44

RESULT 179
ID Q9IJQ1 PRELIMINARY; PRT; 122 AA.
AC Q9IJQ1
RC STRAIN=GP41ERRJ24;
RA Caride E., Hertoghs K., Larder B., Dehertogh P., Brindeiro R.,
RA Machado E., de Sa C.A.M., Eyer W., Passioni L.F.C., Menezes J.A.,
RA Calazans A.R., Tanuri A.;
RT "Genotyping and phenotyping analysis of B and non-B Human
RT immunodeficiency virus type 1 subtypes from patients under HAART.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR ENBL; AF165557; AAF08502.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Transmembrane.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
FT NON_TER 122
SQ SEQUENCE 122 AA; 14635 MW; D052E4B73AE3008E CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 R1LAVERYLKDQQLGIWCSGKLC 26
Db 19 RVLAVERYLKDQQLGIWCSGKLC 44
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DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Envelope glycoprotein gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AR59;
RX MEDLINE=20346416; PubMed=10890362;
RA Masciotra S., Livellara B., Belloso W., Clara L., Tanuri A., Ramos A.,
RA Baggs J., Lal R., Pieniazek D.;
RT "Evidence for a high frequency of HIV-1 subtype F infections among
RT heterosexual population in Buenos Aires, Argentina.";
RL AIDS Res. Hum. Retroviruses 16:1007-1014(2000).
DR ENBL; AF220681; AAF74233.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Transmembrane.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
FT NON_TER 122
SQ SEQUENCE 122 AA; 14676 MW; D2B27F903F4EB2AD CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 R1LAVERYLKDQQLGIWCSGKLC 26
Db 19 RVLAVERYLKDQQLGIWCSGKLC 44

RESULT 180
ID Q9WR01 PRELIMINARY; PRT; 122 AA.
AC Q9WR01
RC STRAIN=97ug398;
RT "Phylogenetic analysis of gp41 envelope of HIV-1 groups M, N, and O
RT isolates provides an alternate region for subtype determination.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR ENBL; AF13581; AAD42749.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Transmembrane.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
FT NON_TER 122
SQ SEQUENCE 122 AA; 14848 MW; FEF3F7555D0D1A63 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 R1LAVERYLKDQQLGIWCSGKLC 26
Db 19 RVLAVERYLKDQQLGIWCSGKLC 44
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RESULT 181
Q91JL1
ID Q91JL1 PRELIMINARY; PRT; 122 AA.
AC Q91JL1;
DT 01-OCT-2000 (TREMELrel. 15, Created)
DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AR47;
RX MEDLINE=20346416; PubMed=10890362;
RA Masciotra S., Livellara B., Bellosso W., Clara L., Tanuri A., Ramos A.,
RA Baggs J., Lal R., Pieniazek D.;
RT "Evidence for a high frequency of HIV-1 subtype F infections among
RT heterosexual population in Buenos Aries, Argentina.";
RL AIDS Res. Hum. Retroviruses 16:1007-1014(2000).
DR EMBL; AF220721; AAF76840.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Transmembrane.
FT NON_TER 1
FT NON_TER 122
FT NON_TER 122
SQ SEQUENCE 122 AA; 14778 MW; 81C07541D00E8C39 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIVGCSGKILIC 26
Db 19 RVLAVERYLKDQQLGIVGCSGKILIC 44

RESULT 182
Q91JL1
ID Q91JL1 PRELIMINARY; PRT; 122 AA.
AC Q91JL1;
DT 01-OCT-2000 (TREMELrel. 15, Created)
DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AR60;
RX MEDLINE=20346416; PubMed=10890362;
RA Masciotra S., Livellara B., Bellosso W., Clara L., Tanuri A., Ramos A.,
RA Baggs J., Lal R., Pieniazek D.;
RT "Evidence for a high frequency of HIV-1 subtype F infections among
RT heterosexual population in Buenos Aries, Argentina.";
RL AIDS Res. Hum. Retroviruses 16:1007-1014(2000).
DR EMBL; AF220703; AAF76822.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Transmembrane.
FT NON_TER 1
FT NON_TER 122
FT NON_TER 122
SQ SEQUENCE 122 AA; 14679 MW; ABE4BB421A98FFA5 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIVGCSGKILIC 26
Db 19 RVLAVERYLKDQQLGIVGCSGKILIC 44

RESULT 183
Q91JQ9
ID Q91JQ9 PRELIMINARY; PRT; 122 AA.
AC Q91JQ9;
DT 01-OCT-2000 (TREMELrel. 15, Created)
DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE Envelope glycoprotein gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AR20;
RX MEDLINE=20346416; PubMed=10890362;
RA Masciotra S., Livellara B., Bellosso W., Clara L., Tanuri A., Ramos A.,
RA Baggs J., Lal R., Pieniazek D.;
RT "Evidence for a high frequency of HIV-1 subtype F infections among
RT heterosexual population in Buenos Aries, Argentina.";
RL AIDS Res. Hum. Retroviruses 16:1007-1014(2000).
DR EMBL; AF220673; AAF74225.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Transmembrane.
FT NON_TER 1
FT NON_TER 122
FT NON_TER 122
SQ SEQUENCE 122 AA; 14757 MW; C342A2EBE4725B3E CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIVGCSGKILIC 26
Db 19 RVLAVERYLKDQQLGIVGCSGKILIC 44

RESULT 184
Q91JF5
ID Q91JF5 PRELIMINARY; PRT; 122 AA.
AC Q91JF5;
DT 01-OCT-2000 (TREMELrel. 15, Created)
DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AR17;
RX MEDLINE=20346416; PubMed=10890362;
RA Masciotra S., Livellara B., Bellosso W., Clara L., Tanuri A., Ramos A.,
RA Baggs J., Lal R., Pieniazek D.;
RT "Evidence for a high frequency of HIV-1 subtype F infections among
RT heterosexual population in Buenos Aries, Argentina.";
RL AIDS Res. Hum. Retroviruses 16:1007-1014(2000).
DR EMBL; AF220687; AAF76806.1; -.
Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIVGCSGKILIC 26
Db 19 RVLAVERYLKDQQLGIVGCSGKILIC 44
```

```
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14749 MW; 8108603A372AABC4 CRC64;

Query Match          99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 R1LAVERYLKDQQLGIWCSGKLIC 26
   |:|||||
Db 19 RVLAVERYLKDQQLGIWCSGKLIC 44

RESULT 185
Q9ILM2 PRELIMINARY; PRT; 122 AA.
AC Q9ILM2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UG275;
RX MEDLINE=20284721; PubMed=10826488;
RA Downing R., Pieniazek D., Hu D.J., Biryahwaho B., Fridlund C.,
RA Rayfield M.A., Sempala S.D., Lal R.B.;
RT "Genetic characterization and phylogenetic analysis of HIV-1 subtype C
RT from Uganda.";
RL AIDS Res. Hum. Retroviruses 16:815-819(2000).
DR EMBL; AF206036; AAF81992.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14768 MW; DED3A42C9DF76D38 CRC64;

Query Match          99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 R1LAVERYLKDQQLGIWCSGKLIC 26
   |:|||||
Db 19 R1LAVERYLKDQQLGIWCSGKLIC 44

RESULT 186
Q90DT2 PRELIMINARY; PRT; 122 AA.
AC Q90DT2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
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RP SEQUENCE FROM N.A.
RC STRAIN=UG;
RA Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,
RA Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;
RT "Similar distribution and continued predominance of HIV-1 subtypes A
RT and D infections in Uganda.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307649; AAL08710.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14713 MW; A6117281CEA10231 CRC64;

Query Match          99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 R1LAVERYLKDQQLGIWCSGKLIC 26
   |:|||||
Db 19 RVLAVERYLKDQQLGIWCSGKLIC 44

RESULT 187
Q9YXP3 PRELIMINARY; PRT; 122 AA.
AC Q9YXP3;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein immunodominant region (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RJ968RFP071;
RA Tanuri A., Swanson P.A., Devare S.G., Berro O.J., Savedra A.,
RA Costa L.J., Telles J.G., Brindeiro R., Schable C., Pieniazek D.,
RA Rayfield M.;
RT "HIV-1 subtypes among blood donors from Rio de Janeiro, Brazil.";
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF034060; AAC79312.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14701 MW; 4EED351A06F7C74F CRC64;

Query Match          99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 R1LAVERYLKDQQLGIWCSGKLIC 26
   |:|||||
Db 19 RVLAVERYLKDQQLGIWCSGKLIC 44

RESULT 188
Q9EA82 PRELIMINARY; PRT; 122 AA.
AC Q9EA82;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
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Db	19	RVLAVERYLKDQQLLGWCSGKLIC	44
RESULT 190			
Q91JQ4			
ID	Q91JQ4	PRELIMINARY;	PRT; 122 AA.
AC	Q91JQ4;		
DT	01-OCT-2000 (T-EMBLrel. 15, Created)		
DT	01-OCT-2000 (T-EMBLrel. 15, Last sequence update)		
DT	01-JUN-2003 (T-EMBLrel. 24, Last annotation update)		
DE	Envelope glycoprotein gp41 (Fragment).		
EN	ENV.		
GS	Human immunodeficiency virus 1.		
OX	Viruses; Retrovird viruses; Retroviridae; Lentivir.		
OC	NCBI_TaxID=11676;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=AR39;		
RX	MEDLINE=20346416; PubMed=10890362;		
RA	Masciotra S., Livellara B., Bellosso W., Clara L., Tanuri A., Ramos A.,		
RA	Baggs J., Lal R., Pieniazek D.;		
RT	"evidence for a high frequency of HIV-1 subtype F infections among		
RT	heterosexual population in Buenos Aires, Argentina.";		
RT	AIDS Res. Hum. Retroviruses 16:1007-1014 (2000).		
RL	EMBL; AF226678; AAF74230.1; -		
DR	GO; GO:0016021; C:integral to membrane; IEA.		
DR	GO; GO:0019031; C:viral envelope; IEA.		
DR	GO; GO:0005198; F:structural molecule activity; IEA.		
DR	InterPro; IPR000328; Env_GP41.		
DR	Pfam; PF00517; GP41; 1.		
DR	Transmembrane.		
FT	NON_TER	1	1
FT	NON_TER	122	122
SQ	SEQUENCE	122 AA; 14703 MW; 834721661D3A360E CRC64;	
Query Match		99.3%; Score 138; DB 15; Length 122;	
Best Local Similarity		96.2%; Pred. No. 1.9e-13;	
Matches 25; Conservative		1; Mismatches 0; Indels 0; Gaps	
Qy	1	RILAVERYLKDQQLLGWCSGKLIC	26
		:-:	
Db	19	RVLAVERYLKDQQLLGWCSGKLIC	44
RESULT 191			
Q90DM3			
ID	Q90DM3	PRELIMINARY;	PRT; 122 AA.
AC	Q90DM3;		
DT	01-DEC-2001 (T-EMBLrel. 19, Created)		
DT	01-DEC-2001 (T-EMBLrel. 19, Last sequence update)		
DT	01-JUN-2003 (T-EMBLrel. 24, Last annotation update)		
DE	Envelope glycoprotein (Fragment).		
EN	ENV.		
GS	Human immunodeficiency virus 1.		
OX	Viruses; Retrovird viruses; Retroviridae; Lentivirus.		
OC	NCBI_TaxID=11676;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=UG;		
RA	Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,		
RA	Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;		
RT	"Similar distribution and continued predominance of HIV-1 subtypes A		
RT	and D infections in Uganda.";		
RL	Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.		
RL	EMBL; AF307708; AAL08769.1; -		
DR	GO; GO:0016021; C:integral to membrane; IEA.		
DR	GO; GO:0019031; C:viral envelope; IEA.		
DR	GO; GO:0005198; F:structural molecule activity; IEA.		
DR	InterPro; IPR000328; Env_GP41.		
DR	Pfam; PF00517; GP41; 1.		
DR	Transmembrane.		
FT	NON_TER	1	1
FT	NON_TER	122	122

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SQ SEQUENCE 122 AA; 14603 MW; 3DDFA4A8CEC96CB7 CRC64;
Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCSGKLC 26
Db 19 RVLAVERYLKDQQLGIWCSGKLC 44

RESULT 192
Q90DL6 PRELIMINARY; PRT; 122 AA.
AC Q90DL6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UG;
RA Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,
RA Birvahwah B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;
RT "Similar distribution and continued predominance of HIV-1 subtypes A
RT and D infections in Uganda.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307715; AAL08776.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_Gp41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 14779 MW; BF277F4FE662C99F CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCSGKLC 26
Db 19 RVLAVERYLKDQQLGIWCSGKLC 44

RESULT 193
Q9WQ24 PRELIMINARY; PRT; 122 AA.
AC Q9WQ24;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GH3;
RA Pieniazek D., Yang C., Lal R.L.;
RT "Phylogenetic analysis of gp41 envelope of HIV-1 groups M, N, and O
RT isolates provides an alternate region for subtype determination.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF113588; AAD42756.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
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DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_Gp41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 14857 MW; 1FC64594F75A207C CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCSGKLC 26
Db 19 RVLAVERYLKDQQLGIWCSGKLC 44

RESULT 194
Q9YXN5 PRELIMINARY; PRT; 122 AA.
AC Q9YXN5;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein immunodominant region (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RJ97BRP105;
RA Tanuri A., Swanson P.A., Devare S.G., Berro O.J., Savedra A.,
RA Costa L.J., Telles J.G., Brindeiro R., Schable C., Pieniazek D.,
RA Rayfield M.;
RT "HIV-1 subtypes among blood donors from Rio de Janeiro, Brazil.";
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF034068; AAC79320.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_Gp41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 14845 MW; EC2A71B0086440C3 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCSGKLC 26
Db 19 RVLAVERYLKDQQLGIWCSGKLC 44

RESULT 195
Q9QIU8 PRELIMINARY; PRT; 122 AA.
AC Q9QIU8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GP41ERRJ23;
RA Caride E., Hertogs K., Larder B., Dehertogh P., Brindeiro R.,
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RA Machado E., de Sa C.A.M., Eyer W., Passioni L.F.C., Menezes J.A.,
RA Calazans A.R., Tanuri A.;
RT "Genotyping and phenotyping analysis of B and non-B Human
RT immunodeficiency virus type 1 subtypes from patients under HAART.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF165556; AA08501.1; -.
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0019031; C: viral envelope; IEA.
DR GO: GO:0005198; F: structural molecule activity; IEA.
DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00517; GP41; 1.
KW Transmembrane.
KW NON_TER 1
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 14733 MW; 91CD821BA7A7FFCB CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSKLIC 26
|:|||||
Db 19 RVLAVERYLKDQQLGIWCGSKLIC 44

RESULT 196
Q90DN8 PRELIMINARY; PRT; 122 AA.
ID Q90DN8
AC Q90DN8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN SEQUENCE FROM N.A.
RC STRAIN=UG;
RA Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,
RA Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;
RT "Similar distribution and continued predominance of HIV-1 subtypes A
RT and D infections in Uganda.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF307693; AAL08754.1; -.
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0019031; C: viral envelope; IEA.
DR GO: GO:0005198; F: structural molecule activity; IEA.
DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00517; GP41; 1.
KW Transmembrane.
KW NON_TER 1
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 14719 MW; B1A827E231D3748D CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSKLIC 26
|:|||||
Db 19 RVLAVERYLKDQQLGIWCGSKLIC 44

RESULT 197
Q90DN5 PRELIMINARY; PRT; 122 AA.
ID Q90DN5
AC Q90DN5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN SEQUENCE FROM N.A.
RC STRAIN=UG;
RA Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,
RA Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;
RT "Similar distribution and continued predominance of HIV-1 subtypes A
RT and D infections in Uganda.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF307693; AAL08754.1; -.
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0019031; C: viral envelope; IEA.
DR GO: GO:0005198; F: structural molecule activity; IEA.
DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00517; GP41; 1.
KW Transmembrane.
KW NON_TER 1
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 14719 MW; B1A827E231D3748D CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSKLIC 26
|:|||||
Db 19 RVLAVERYLKDQQLGIWCGSKLIC 44

RESULT 198
Q91JP7 PRELIMINARY; PRT; 122 AA.
ID Q91JP7
AC Q91JP7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN SEQUENCE FROM N.A.
RC STRAIN=AR11;
RA Masclotra S., Livellara B., Belloso W., Clara L., Tanuri A., Ramos A.,
RA Baggs J., Lal R., Pieniazek D.;
RT "Evidence for a high frequency of HIV-1 subtype F infections among
RT heterosexual population in Buenos Aires, Argentina.";
RL AIDS Res. Hum. Retroviruses 16:1007-1014 (2000).
DR EMBL: AF220685; AAF74237.1; -.
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0019031; C: viral envelope; IEA.
DR GO: GO:0005198; F: structural molecule activity; IEA.
DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00517; GP41; 1.
KW Transmembrane.
KW NON_TER 1
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 14704 MW; 5538AD9D2B012589 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSKLIC 26
|:|||||
Db 19 RVLAVERYLKDQQLGIWCGSKLIC 44
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GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN SEQUENCE FROM N.A.
RC STRAIN=UG;
RA Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,
RA Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;
RT "Similar distribution and continued predominance of HIV-1 subtypes A
RT and D infections in Uganda.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF307696; AAL08757.1; -.
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0019031; C: viral envelope; IEA.
DR GO: GO:0005198; F: structural molecule activity; IEA.
DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00517; GP41; 1.
KW Transmembrane.
KW NON_TER 1
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 14738 MW; 28669DBD00E3693E CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSKLIC 26
|:|||||
Db 19 RVLAVERYLKDQQLGIWCGSKLIC 44

RESULT 198
Q91JP7 PRELIMINARY; PRT; 122 AA.
ID Q91JP7
AC Q91JP7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN SEQUENCE FROM N.A.
RC STRAIN=AR11;
RA Masclotra S., Livellara B., Belloso W., Clara L., Tanuri A., Ramos A.,
RA Baggs J., Lal R., Pieniazek D.;
RT "Evidence for a high frequency of HIV-1 subtype F infections among
RT heterosexual population in Buenos Aires, Argentina.";
RL AIDS Res. Hum. Retroviruses 16:1007-1014 (2000).
DR EMBL: AF220685; AAF74237.1; -.
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0019031; C: viral envelope; IEA.
DR GO: GO:0005198; F: structural molecule activity; IEA.
DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00517; GP41; 1.
KW Transmembrane.
KW NON_TER 1
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 14704 MW; 5538AD9D2B012589 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSKLIC 26
|:|||||
Db 19 RVLAVERYLKDQQLGIWCGSKLIC 44
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RESULT 199

Q90DL2 ID Q90DL2 PRELIMINARY; PRT; 122 AA.
AC Q90DL2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UG;
RA Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C., Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;
RT "Similar distribution and continued predominance of HIV-1 subtypes A and D infections in Uganda";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307719; AAL08780.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Transmembrane.
KW Envelope protein.
FT NON_TER 1 1
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 14662 MW; 86300081CAC9AA3A CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;

Best Local Similarity 96.2%; Pred.No. 1.9e-13;

Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCSGKLC 26
DB 19 RVLAVERYLKDQQLGIWCSGKLC 44

RESULT 200

Q7ZJS6 ID Q7ZJS6 PRELIMINARY; PRT; 122 AA.
AC Q7ZJS6;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UG95-327;
RA Swanson P.A., Devare S.G., Hackett J.R. Jr.;
RT "Molecular Characterization of 39 HIV-1 Isolates Representing Group M (Subtypes A-G) and Group O: Sequence Analysis of gag p24, pol integrase, and env gp41";
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY214083; AAO61803.1; -
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Envelope protein.
FT NON_TER 1 1
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 14748 MW; 68F48CCA8DC1DBC0 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;

Best Local Similarity 96.2%; Pred.No. 1.9e-13;

Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCSGKLC 26
DB 19 RVLAVERYLKDQQLGIWCSGKLC 44

RESULT 201

Q7ZJS2 ID Q7ZJS2 PRELIMINARY; PRT; 122 AA.
AC Q7ZJS2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UG95-422;
RA Swanson P.A., Devare S.G., Hackett J.R. Jr.;
RT "Molecular Characterization of 39 HIV-1 Isolates Representing Group M (Subtypes A-G) and Group O: Sequence Analysis of gag p24, pol integrase, and env gp41";
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY214087; AAO61807.1; -
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Envelope protein.
FT NON_TER 1 1
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 14675 MW; 4E83B592C7C10ACB CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;

Best Local Similarity 96.2%; Pred.No. 1.9e-13;

Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCSGKLC 26
DB 19 RVLAVERYLKDQQLGIWCSGKLC 44

RESULT 202

Q7ZJS1 ID Q7ZJS1 PRELIMINARY; PRT; 122 AA.
AC Q7ZJS1;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BK132;
RA Swanson P.A., Devare S.G., Hackett J.R. Jr.;
RT "Molecular Characterization of 39 HIV-1 Isolates Representing Group M (Subtypes A-G) and Group O: Sequence Analysis of gag p24, pol integrase, and env gp41";
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY214088; AAO61808.1; -
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Envelope protein.
FT NON_TER 1 1
FT NON_TER 122 122

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SQ SEQUENCE 122 AA; 14674 MW; 95E8C3532B34165F CRC64;
Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSGKLC 26
19 RVLAVERYLKDQQLGIWCGSGKLC 44

RESULT 203
Q7ZJS0
ID Q7ZJS0 PRELIMINARY; PRT; 122 AA.
AC Q7ZJS0;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BZ167;
RA Swanson P.A., Devare S.G., Hackett J.R. Jr.;
RT "Molecular Characterization of 39 HIV-1 Isolates Representing Group M (Subtypes A-G) and Group O: Sequence Analysis of gag p24, pol integrase, and env gp41.";
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY214089; AAO61809.1; -.
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Envelope protein.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14759 MW; 9548FEAC44CD741E CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSGKLC 26
19 RVLAVERYLKDQQLGIWCGSGKLC 44

RESULT 204
Q7ZJR8
ID Q7ZJR8 PRELIMINARY; PRT; 122 AA.
AC Q7ZJR8;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TH1600;
RA Swanson P.A., Devare S.G., Hackett J.R. Jr.;
RT "Molecular Characterization of 39 HIV-1 Isolates Representing Group M (Subtypes A-G) and Group O: Sequence Analysis of gag p24, pol integrase, and env gp41.";
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY214091; AAO61811.1; -.
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
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DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Envelope protein.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14786 MW; 6C4FAFF8579F9104 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSGKLC 26
19 RVLAVERYLKDQQLGIWCGSGKLC 44

RESULT 205
Q7ZJR7
ID Q7ZJR7 PRELIMINARY; PRT; 122 AA.
AC Q7ZJR7;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=US1;
RA Swanson P.A., Devare S.G., Hackett J.R. Jr.;
RT "Molecular Characterization of 39 HIV-1 Isolates Representing Group M (Subtypes A-G) and Group O: Sequence Analysis of gag p24, pol integrase, and env gp41.";
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY214092; AAO61812.1; -.
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Envelope protein.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14748 MW; 08FF40E09139D71E CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSGKLC 26
19 RVLAVERYLKDQQLGIWCGSGKLC 44

RESULT 206
Q7ZJR6
ID Q7ZJR6 PRELIMINARY; PRT; 122 AA.
AC Q7ZJR6;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=US2;
RA Swanson P.A., Devare S.G., Hackett J.R. Jr.;
RT "Molecular Characterization of 39 HIV-1 Isolates Representing Group M (Subtypes A-G) and Group O: Sequence Analysis of gag p24, pol
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RT integrase, and env gp41.";
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY214093; AAO61813.1; -
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Envelope protein.
FT NON TER 1 1
FT NON TER 122 122
SQ SEQUENCE 122 AA; 14767 MW; 038D675003BEC8A5 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIGCSGKLC 26
|:|||||
Db 19 RVLAVERYLKDQQLGIGCSGKLC 44

RESULT 207

ID Q7ZJR5 PRELIMINARY; PRT; 122 AA.
AC Q7ZJR5;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.

OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=US3;
RA Swanson P.A., Devare S.G., Hackett J.R. Jr.;
RT "Molecular Characterization of 39 HIV-1 Isolates Representing Group M (Subtypes A-G) and Group O: Sequence Analysis of gag p24, pol integrase, and env gp41.";
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY214094; AAO61814.1; -
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.

KW Envelope protein.
FT NON TER 1 1
FT NON TER 122 122
SQ SEQUENCE 122 AA; 14822 MW; 3732E22879944B0D CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIGCSGKLC 26
|:|||||
Db 19 RVLAVERYLKDQQLGIGCSGKLC 44

RESULT 208

ID Q7ZJP0 PRELIMINARY; PRT; 122 AA.
AC Q7ZJP0;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.

OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=IVCO3671;
RA Swanson P.A., Devare S.G., Hackett J.R. Jr.;
RT "Molecular Characterization of 39 HIV-1 Isolates Representing Group M (Subtypes A-G) and Group O: Sequence Analysis of gag p24, pol integrase, and env gp41.";
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY214119; AAO61839.1; -
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Envelope protein.
FT NON TER 1 1
FT NON TER 122 122
SQ SEQUENCE 122 AA; 14762 MW; 7272AD069B69B689 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIGCSGKLC 26
|:|||||
Db 19 RVLAVERYLKDQQLGIGCSGKLC 44

RESULT 209

ID Q8J3S3 PRELIMINARY; PRT; 123 AA.
AC Q8J3S3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN ENV.

OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.

RA Esteves A., Parreira R., Venenno T., Franco M., Piedade J.,
de Sousa G., Canas-Ferreira W.;
RT "Molecular epidemiology of HIV-1 infection in Portugal: high prevalence of non-B subtypes.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ318398; CAC85977.1; -
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.

KW Transmembrane.
FT NON TER 1 1
FT NON TER 123 123
SQ SEQUENCE 123 AA; 14914 MW; C94786EC61260642 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 123;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIGCSGKLC 26
|:|||||
Db 17 RVLAVERYLKDQQLGIGCSGKLC 42

RESULT 210

ID Q8J3R5 PRELIMINARY; PRT; 123 AA.
AC Q8J3R5;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).

```
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Esteves A., Parreira R., Venenno T., Franco M., Piedade J.,
RA de Sousa G., Canas-Ferreira W.;
RT "Molecular epidemiology of HIV-1 infection in Portugal: high
RT prevalence of non-B subtypes.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ318406; CAC85985.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Transmembrane.
KW NON_TER 1
FT NON_TER 123 123
SQ SEQUENCE 123 AA; 14897 MW; 5D37383E8DCCE8E0 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 123;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSGKLC 26
Db 17 RVLAVERYLKDQQLGIWCGSGKLC 42

RESULT 211
QYXR3 PRELIMINARY; PRT; 123 AA.
AC QYXR3;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein immunodominant region (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Tanuri A., Swanson P.A., Devare S.G., Berro O.J., Savedra A.,
RA Costa L.J., Telles J.G., Brindeiro R., Schable C., Pieniazek D.,
RA Rayfield M.;
RT "HIV-1 subtypes among blood donors from Rio de Janeiro, Brazil.";
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF034040; AAC79292.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Transmembrane.
KW NON_TER 1
FT NON_TER 123 123
SQ SEQUENCE 123 AA; 14791 MW; D79184FA768C0E60 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 123;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSGKLC 26
Db 19 RVLAVERYLKDQQLGIWCGSGKLC 44

RESULT 212
QYXR3 PRELIMINARY; PRT; 123 AA.
AC QYXR3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Esteves A., Parreira R., Venenno T., Franco M., Piedade J.,
RA de Sousa G., Canas-Ferreira W.;
RT "Molecular epidemiology of HIV-1 infection in Portugal: high
RT prevalence of non-B subtypes.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ318399; CAC85978.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Transmembrane.
KW NON_TER 1
FT NON_TER 123 123
SQ SEQUENCE 123 AA; 14862 MW; 0F1E4342A90F42C9 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 123;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSGKLC 26
Db 17 RVLAVERYLKDQQLGIWCGSGKLC 42

RESULT 213
QYXR3 PRELIMINARY; PRT; 123 AA.
AC QYXR3;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Esteves A., Parreira R., Venenno T., Franco M., Piedade J.,
RA Germano de Sousa J., Canas-Ferreira W.;
RT "Genetic diversity of HIV-1 spreading among intravenous drug users in
RT Lisbon, Portugal.";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ429042; CAD23678.1; -.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Transmembrane.
KW NON_TER 1
FT NON_TER 123 123
SQ SEQUENCE 123 AA; 14883 MW; 17C6F08AB45DF8FA CRC64;

Query Match 99.3%; Score 138; DB 15; Length 123;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSGKLC 26
Db 17 RVLAVERYLKDQQLGIWCGSGKLC 42
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RESULT 214
Q8J3R7
ID Q8J3R7 PRELIMINARY; PRT; 124 AA.
AC Q8J3R7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Esteves A., Parreira R., Venenno T., Franco M., Piedade J.,
de Sousa G., Canas-Ferreira W.;
RT "Molecular epidemiology of HIV-1 infection in Portugal: high
prevalence of non-B subtypes.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ318404; CAC85983.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_Gp41.
DR Pfam; PF00517; GP41; 1.
DR Transmembrane.
FT NON_TER 1
FT NON_TER 124
FT SEQUENCE 124 AA; 14833 MW; 1373000B4D60F5A CRC64;

Query Match 99.3%; Score 138; DB 15; Length 124;
Best Local Similarity 96.2%; Pred. No. 2e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGWCSGKLC 26
Db 18 RVLAVERYLKDQQLGWCSGKLC 43

RESULT 215
Q9YZ03
ID Q9YZ03 PRELIMINARY; PRT; 124 AA.
AC Q9YZ03;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=140.223;
RA Brennan C.A., Lund J.K., Golden A., Yamaguchi J., Vallari A.S.,
Phillips J.F., Kataaha P.K., Jackson J.B., Devate S.G.;
RT "Serologic and Phylogenetic Characterization of HIV-1 Subtypes in
Uganda.";
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF006866; AAD01310.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_Gp41.
DR Pfam; PF00517; GP41; 1.
DR Transmembrane.
FT NON_TER 1
FT NON_TER 124
FT SEQUENCE 124 AA; 14820 MW; 37C85D6A080B393B CRC64;

Query Match 99.3%; Score 138; DB 15; Length 124;
Best Local Similarity 96.2%; Pred. No. 2e-13;

Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGWCSGKLC 26
Db 18 RVLAVERYLKDQQLGWCSGKLC 43

RESULT 216
Q9IWP9
ID Q9IWP9 PRELIMINARY; PRT; 125 AA.
AC Q9IWP9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=85CD244;
RX MEDLINE=21134754; PubMed=11242522;
RA Yang C., Dash B., Hanna S.L., Frances H.S., Nzilambi N.,
Colebunders R.C., St Louis M., Quinn T.C., Folks T.M., Lal R.B.;
RT "Predominance of HIV type 1 subtype G among commercial sex workers
from Kinshasa, Democratic Republic of Congo.";
RL AIDS Res. Hum. Retroviruses 17:361-365(2001).
DR EMBL; AF260477; RAF71944.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_Gp41.
DR Pfam; PF00517; GP41; 1.
DR Transmembrane.
FT NON_TER 1
FT NON_TER 125
FT SEQUENCE 125 AA; 14805 MW; 4EB9BF1C23F33469 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 125;
Best Local Similarity 96.2%; Pred. No. 2e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGWCSGKLC 26
Db 33 RVLAVERYLKDQQLGWCSGKLC 58

RESULT 217
Q9IWP9
ID Q9IWP9 PRELIMINARY; PRT; 126 AA.
AC Q9IWP9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=85CD116;
RX MEDLINE=21134754; PubMed=11242522;
RA Yang C., Dash B., Hanna S.L., Frances H.S., Nzilambi N.,
Colebunders R.C., St Louis M., Quinn T.C., Folks T.M., Lal R.B.;
RT "Predominance of HIV type 1 subtype G among commercial sex workers
from Kinshasa, Democratic Republic of Congo.";
RL AIDS Res. Hum. Retroviruses 17:361-365(2001).
DR EMBL; AF260467; RAF71934.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
```

```
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 126
FT NON_TER 126
SQ SEQUENCE 126 AA; 15246 MW; A73CDEFAAC6E129 CRC64;

Query Match
Best Local Similarity 99.3%; Score 138; DB 15; Length 126;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSGKLC 26
Db 17 RVLAVERYLKDQQLGIWCGSGKLC 42

RESULT 218
Q9YX6 PRELIMINARY; PRT; 127 AA.
AC Q9YX6;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE GP41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=264.643;
RA Brennan C.A., Lund J.K., Golden A., Yamaguchi J., Vallari A.S.,
RA Phillips J.F., Kataaha P.K., Jackson J.B., Devare S.G.;
RT "Serologic and Phylogenetic Characterization of HIV-1 Subtypes in
RT Uganda.";
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF06923; AAD01367.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 127
FT NON_TER 127
SQ SEQUENCE 127 AA; 15335 MW; A3422CAD00B2CFB7 CRC64;

Query Match
Best Local Similarity 99.3%; Score 138; DB 15; Length 127;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSGKLC 26
Db 25 RVLAVERYLKDQQLGIWCGSGKLC 50

RESULT 219
Q9IWR0 PRELIMINARY; PRT; 127 AA.
AC Q9IWR0;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=85CD085;
RX MEDLINE=21134754; PubMed=11242522;
RA Yang C., Dash B., Hanna S.L., Frances H.S., Nzilambi N.,

RA Colebunders R.C., St Louis M., Quinn T.C., Folks T.M., Lal R.B.;
RT "Predominance of HIV type 1 subtype G among commercial sex workers
RT from Kinshasa, Democratic Republic of Congo.";
RL AIDS Res. Hum. Retroviruses 17:361-365(2001).
DR EMBL; AF260466; AAF71933.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 127
FT NON_TER 127
SQ SEQUENCE 127 AA; 15272 MW; 076E4A6CBA8B822E CRC64;

Query Match
Best Local Similarity 99.3%; Score 138; DB 15; Length 127;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSGKLC 26
Db 19 RVLAVERYLKDQQLGIWCGSGKLC 44

RESULT 220
Q9WM82 PRELIMINARY; PRT; 127 AA.
AC Q9WM82;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE GP41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=122.335;
RA Brennan C.A., Lund J.K., Golden A., Yamaguchi J., Vallari A.S.,
RA Phillips J.F., Kataaha P.K., Jackson J.B., Devare S.G.;
RT "Serologic and Phylogenetic Characterization of HIV-1 Subtypes in
RT Uganda.";
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF006846; AAD01290.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 127
FT NON_TER 127
SQ SEQUENCE 127 AA; 15296 MW; 6F8361B317B554CA CRC64;

Query Match
Best Local Similarity 99.3%; Score 138; DB 15; Length 127;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSGKLC 26
Db 25 RVLAVERYLKDQQLGIWCGSGKLC 50

RESULT 221
Q9WM85 PRELIMINARY; PRT; 127 AA.
AC Q9WM85;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE GP41 (Fragment).
GN ENV.
```

ID	Q9IHY1	PRELIMINARY;	PRT;	128 AA.
DT	Q9IHY1;			
DT	01-OCT-2000	(TrEMBLrel. 15, Created)		
DT	01-OCT-2000	(TrEMBLrel. 15, Last sequence update)		
DT	01-JUN-2003	(TrEMBLrel. 24, Last annotation update)		
DE	Envelope glycoprotein. (Fragment).			
GN	ENV.			
OS	Human immunodeficiency virus 1.			
OC	Viruses; Retrovirdae; Retroviridae; Lentivirus.			
NCBI_TaxID=11676;	[1]			
RN	SEQUENCE FROM N.A.			
RC	STRAIN=98CMO10;			
RX	MEDLINE=20386754;	PubMed=10933623;		
RA	Yang C., Gao F., Fonjundo P.N., Zekeng L., van der Groen G., Pleniakzek D., Schable C., Lal R.B.;	"Phylogenetic analysis of protease and transmembrane regions of HIV type 1 group O.";		
RT	AIDS Res. Hum. Retroviruses 16:1075-1081(2000).			
RL	ENBL; AF229203; AAF71457.1; -.			
DR	GO; GO:0016021; C:integral to membrane; IEA.			
DR	GO; GO:0019031; C:viral envelope; IEA.			
DR	GO; GO:0005198; F:structural molecule activity; IEA.			
DR	InterPro; IPR000328; Env_GP41.			
DR	Fam; PF00517; GP41; 1.			
KW	Transmembrane.			
FT	NON_TER	1		
FT	NON_TER	128		
FT	NON_TER	128		
SQ	SEQUENCE	128 AA; 15459 MW; B04136F4362EFB27 CRC64;		
 Query Match 99.3%; Score 138; DB 15; Length 128; Best Local Similarity 96.2%; Pred. No. 2e-13; Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;				
QY	1 RLAVERYLKDQQLGICSGKLC 26 :			
Dd	25 RVLAVERYLKDQQLGICSGKLC 50 :			
 RESULT 224				
Q9YZO				
ID	Q9YZO	PRELIMINARY;	PRT;	129 AA.
AC	Q9YZO;			
DT	01-MAY-1999	(TrEMBLrel. 10, Created)		
DT	01-MAY-1999	(TrEMBLrel. 10, Last sequence update)		
DT	01-JUN-2003	(TrEMBLrel. 24, Last annotation update)		
DE	Gp41 (Fragment).			
GN	ENV.			
OS	Human immunodeficiency virus 1.			
OC	Viruses; Retrovirdae; Retroviridae; Lentivirus.			
NCBI_TaxID=11676;	[1]			
RN	SEQUENCE FROM N.A.			
RC	STRAIN=225.318;			
RA	Brennan C.A., Lund J.K., Golden A., Yamaguchi J., Vallari A.S., Phillips J.F., Kataaha P.K., Jackson J.B., Devare S.G.;	"Serologic and Phylogenetic Characterization of HIV-1 Subtypes in Uganda."		
RT	Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.			
RL	ENBL; AF006898; AAD01342.1; -.			
DR	GO; GO:0016021; C:integral to membrane; IEA.			
DR	GO; GO:0019031; C:viral envelope; IEA.			
DR	GO; GO:0005198; F:structural molecule activity; IEA.			
DR	InterPro; IPR000328; Env_GP41.			
DR	Fam; PF00517; GP41; 1.			
KW	Transmembrane.			
FT	NON_TER	1		
FT	NON_TER	129		
FT	NON_TER	129		
SQ	SEQUENCE	129 AA; 15523 MW; 433A3AF534C73CD7 CRC64;		
 Query Match 99.3%; Score 138; DB 15; Length 129; Best Local Similarity 96.2%; Pred. No. 2e-13; Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;				

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Qy 1 RILAVERYLKDQQLGIWCGSKLIC 26
Db 26 RVLAVERYLKDQQLGIWCGSKLIC 51

RESULT 225
Q9YYV2 Q9YYV2 PRELIMINARY; PRT; 129 AA.
AC Q9YYV2
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=230.298;
RA Brennan C.A., Lund J.K., Golden A., Yamaguchi J., Vallari A.S.,
RA Phillips J.F., Kataaha P.K., Jackson J.B., Devare S.G.;
RT "Serologic and Phylogenetic Characterization of HIV-1 Subtypes in
RT Uganda.";
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF06912; AAD01356.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 129
SQ SEQUENCE 129 AA; 15469 MW; 3B952B1A2D229808 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 129;
Best Local Similarity 96.2%; Pred. No. 2e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RILAVERYLKDQQLGIWCGSKLIC 26
Db 26 RVLAVERYLKDQQLGIWCGSKLIC 51

RESULT 226
Q9IWR6 Q9IWR6 PRELIMINARY; PRT; 130 AA.
AC Q9IWR6;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=85CD246;
RA Yang C., Dash B., Hanna S.L., Frances H.S., Nzilambi N.,
RA Colebunders R.C., St Louis M., Quinn T.C., Folks T.M., Lal R.B.;
RT "Predominance of HIV type 1 subtype G among commercial sex workers
RT from Kinshasa, Democratic Republic of Congo.";
RL AIDS Res. Hum. Retroviruses 17:361-365(2001).
DR EMBL; AF260460; AAF71927.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.

Qy 1 RILAVERYLKDQQLGIWCGSKLIC 26
Db 27 RVLAVERYLKDQQLGIWCGSKLIC 52

RESULT 227
Q9IYW6 Q9IYW6 PRELIMINARY; PRT; 130 AA.
AC Q9IYW6;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=326.662;
RA Brennan C.A., Lund J.K., Golden A., Yamaguchi J., Vallari A.S.,
RA Phillips J.F., Kataaha P.K., Jackson J.B., Devare S.G.;
RT "Serologic and Phylogenetic Characterization of HIV-1 Subtypes in
RT Uganda.";
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF006941; AAD01385.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 130
SQ SEQUENCE 130 AA; 15581 MW; 7652D93F692D2527 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 130;
Best Local Similarity 96.2%; Pred. No. 2.1e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RILAVERYLKDQQLGIWCGSKLIC 26
Db 27 RVLAVERYLKDQQLGIWCGSKLIC 52

RESULT 228
Q9IYW0 Q9IYW0 PRELIMINARY; PRT; 132 AA.
AC Q9IYW0;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=85CD225;
RA Yang C., Dash B., Hanna S.L., Frances H.S., Nzilambi N.,
RA Colebunders R.C., St Louis M., Quinn T.C., Folks T.M., Lal R.B.;
RT "Predominance of HIV type 1 subtype G among commercial sex workers
```

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KW Transmembrane.
FT NON_TER 1
FT NON_TER 130
SQ SEQUENCE 130 AA; 15662 MW; 33C9EE30DA2A98C4 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 130;
Best Local Similarity 96.2%; Pred. No. 2.1e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RILAVERYLKDQQLGIWCGSKLIC 26
Db 20 RVLAVERYLKDQQLGIWCGSKLIC 45

RESULT 227
Q9IYW6 Q9IYW6 PRELIMINARY; PRT; 130 AA.
AC Q9IYW6;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=326.662;
RA Brennan C.A., Lund J.K., Golden A., Yamaguchi J., Vallari A.S.,
RA Phillips J.F., Kataaha P.K., Jackson J.B., Devare S.G.;
RT "Serologic and Phylogenetic Characterization of HIV-1 Subtypes in
RT Uganda.";
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF006941; AAD01385.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 130
SQ SEQUENCE 130 AA; 15581 MW; 7652D93F692D2527 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 130;
Best Local Similarity 96.2%; Pred. No. 2.1e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RILAVERYLKDQQLGIWCGSKLIC 26
Db 27 RVLAVERYLKDQQLGIWCGSKLIC 52

RESULT 228
Q9IYW0 Q9IYW0 PRELIMINARY; PRT; 132 AA.
AC Q9IYW0;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=85CD225;
RA Yang C., Dash B., Hanna S.L., Frances H.S., Nzilambi N.,
RA Colebunders R.C., St Louis M., Quinn T.C., Folks T.M., Lal R.B.;
RT "Predominance of HIV type 1 subtype G among commercial sex workers
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RT from Kinshasa, Democratic Republic of Congo.";
RL AIDS Res. Hum. Retroviruses 17:361-365 (2001).
DR EMBL; AF260476; AAF71943.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 132
SQ SEQUENCE 132 AA; 15607 MW; 6A05003B8A9F2B14 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 132;
Best Local Similarity 96.2%; Pred. No. 2.1e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 R1LAVERYLKDQQLGIGWCSGKLC 26
DB 35 RVLAVERYLKDQQLGIGWCSGKLC 60

RESULT 229
Q8UQZ6 PRELIMINARY; PRT; 133 AA.
AC Q8UQZ6;
RX MEDLINE=21602569; PubMed=11739704;
RA Trask S.A., Derdeyn C.A., Fideli U., Chen Y., Meleth S., Kasolo F.,
RA Musonda R., Hunter E., Gao F., Allen S., Hahn B.H.;
RT "Molecular epidemiology of human immunodeficiency virus type 1
RT transmission in a heterosexual cohort of discordant couples in
RT Zambia.";
RL J. Virol. 76:397-405 (2002).
DR EMBL; AF405187; AAL66700.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 133
SQ SEQUENCE 133 AA; 15827 MW; 5AD3D0BAA789780B CRC64;

Query Match 99.3%; Score 138; DB 15; Length 133;
Best Local Similarity 96.2%; Pred. No. 2.1e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 R1LAVERYLKDQQLGIGWCSGKLC 26
DB 27 RVLAVERYLKDQQLGIGWCSGKLC 52

RESULT 231
Q9YZ13 PRELIMINARY; PRT; 133 AA.
AC Q9YZ13;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE GP41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1];
RP SEQUENCE FROM N.A.
RC STRAIN=127.568;
RA Brennan C.A., Lund J.K., Golden A., Yamaguchi J., Vallari A.S.,
RA Phillips J.F., Kataaha P.K., Jackson J.B., Devare S.G.;
RT "Serologic and Phylogenetic Characterization of HIV-1 Subtypes in
RT Uganda.";
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF008850; AAD01294.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 133
SQ SEQUENCE 133 AA; 15931 MW; 184000DE0606C81 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 133;
Best Local Similarity 96.2%; Pred. No. 2.1e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 R1LAVERYLKDQQLGIGWCSGKLC 26
DB 29 RVLAVERYLKDQQLGIGWCSGKLC 54

RESULT 230
Q8UQW8 PRELIMINARY; PRT; 133 AA.
AC Q8UQW8;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.

from Kinshasa, Democratic Republic of Congo.";
RL AIDS Res. Hum. Retroviruses 17:361-365 (2001).
DR EMBL; AF260476; AAF71943.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 132
SQ SEQUENCE 132 AA; 15607 MW; 6A05003B8A9F2B14 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 132;
Best Local Similarity 96.2%; Pred. No. 2.1e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 R1LAVERYLKDQQLGIGWCSGKLC 26
DB 35 RVLAVERYLKDQQLGIGWCSGKLC 60

RESULT 229
Q8UQZ6 PRELIMINARY; PRT; 133 AA.
AC Q8UQZ6;
RX MEDLINE=21602569; PubMed=11739704;
RA Trask S.A., Derdeyn C.A., Fideli U., Chen Y., Meleth S., Kasolo F.,
RA Musonda R., Hunter E., Gao F., Allen S., Hahn B.H.;
RT "Molecular epidemiology of human immunodeficiency virus type 1
RT transmission in a heterosexual cohort of discordant couples in
RT Zambia.";
RL J. Virol. 76:397-405 (2002).
DR EMBL; AF405187; AAL66700.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 133
SQ SEQUENCE 133 AA; 16145 MW; 6DBD34C92AFDA77D CRC64;

Query Match 99.3%; Score 138; DB 15; Length 133;
Best Local Similarity 96.2%; Pred. No. 2.1e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 R1LAVERYLKDQQLGIGWCSGKLC 26
DB 27 RVLAVERYLKDQQLGIGWCSGKLC 52

RESULT 230
Q8UQW8 PRELIMINARY; PRT; 133 AA.
AC Q8UQW8;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
```

```
RESULT 232
Q90Q18 ID Q90Q18 PRELIMINARY; PRT; 133 AA.
AC Q90Q18;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RC STRAIN=99ES-MOI157;
RX MEDLINE=21322034; PubMed=11429126;
RA Ortiz M., Sanchez I., Gonzalez M.P., Leon M.I., Abeso N., Asumu E.,
RA Garcia-Saiz A.;
RT "Molecular epidemiology of HIV type 1 subtypes in Equatorial Guinea.";
RL AIDS Res. Hum. Retroviruses 17:851-855(2001).
DR EMBL; AF331123; AAK92334.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Transmembrane.
FT NON_TER 1
FT NON_TER 133
FT NON_TER 133
SQ SEQUENCE 133 AA; 15612 MW; 84142CA9E98813E6 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 133;
Best Local Similarity 96.2%; Pred. No. 2.1e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLAVERYLKDQQLGIWCSGKLC 26
Db 36 RVLAVERYLKDQQLGIWCSGKLC 61

RESULT 233
Q90Q57 ID Q90Q57 PRELIMINARY; PRT; 133 AA.
AC Q90Q57;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RC STRAIN=99ES-MOI1475;
RX MEDLINE=21322034; PubMed=11429126;
RA Ortiz M., Sanchez I., Gonzalez M.P., Leon M.I., Abeso N., Asumu E.,
RA Garcia-Saiz A.;
RT "Molecular epidemiology of HIV type 1 subtypes in Equatorial Guinea.";
RL AIDS Res. Hum. Retroviruses 17:851-855(2001).
DR EMBL; AF331084; AAK92295.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Transmembrane.
FT NON_TER 1
FT NON_TER 133
FT NON_TER 133
SQ SEQUENCE 133 AA; 15765 MW; 8534092BDE8ADB4F CRC64;

Query Match 99.3%; Score 138; DB 15; Length 133;
Best Local Similarity 96.2%; Pred. No. 2.1e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLAVERYLKDQQLGIWCSGKLC 26
Db 36 RVLAVERYLKDQQLGIWCSGKLC 61

RESULT 234
Q90Q63 ID Q90Q63 PRELIMINARY; PRT; 133 AA.
AC Q90Q63;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RC STRAIN=99ES-MOI1468;
RX MEDLINE=21322034; PubMed=11429126;
RA Ortiz M., Sanchez I., Gonzalez M.P., Leon M.I., Abeso N., Asumu E.,
RA Garcia-Saiz A.;
RT "Molecular epidemiology of HIV type 1 subtypes in Equatorial Guinea.";
RL AIDS Res. Hum. Retroviruses 17:851-855(2001).
DR EMBL; AF331078; AAK92289.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Transmembrane.
FT NON_TER 1
FT NON_TER 133
FT NON_TER 133
SQ SEQUENCE 133 AA; 15774 MW; 8F84BF80B2EF26F8 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 133;
Best Local Similarity 96.2%; Pred. No. 2.1e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLAVERYLKDQQLGIWCSGKLC 26
Db 36 RVLAVERYLKDQQLGIWCSGKLC 61

RESULT 235
Q90P23 ID Q90P23 PRELIMINARY; PRT; 133 AA.
AC Q90P23;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RC STRAIN=99ES-MOI1617;
RX MEDLINE=21322034; PubMed=11429126;
RA Ortiz M., Sanchez I., Gonzalez M.P., Leon M.I., Abeso N., Asumu E.,
RA Garcia-Saiz A.;
RT "Molecular epidemiology of HIV type 1 subtypes in Equatorial Guinea.";
RL AIDS Res. Hum. Retroviruses 17:851-855(2001).
DR EMBL; AF331148; AAK92359.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
```

```
KW Transmembrane. 1
FT NON_TER 133
FT NON_TER 133
SQ SEQUENCE 133 AA; 15648 MW; 13A163CF35C3D6F2 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 133;
Best Local Similarity 96.2%; Pred. No. 2.1e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLLGWCSGKLC 26
   |:|||||
Db 36 RVLAVERYLKDQQLLGWCSGKLC 61
   |:|||||

RESULT 236
Q90Q37 PRELIMINARY; PRT; 133 AA.
AC Q90Q37;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=99ES-MO1517;
RX MEDLINE=21322034; PubMed=11429126;
RA Ortiz M., Sanchez I., Gonzalez M.P., Leon M.I., Abeso N., Asumu E.,
RA Garcia-Saiz A.;
RT "Molecular epidemiology of HIV type 1 subtypes in Equatorial Guinea.";
RL AIDS Res. Hum. Retroviruses 17:851-855(2001).
DR EMBL; AF331104; AAK92315.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 133
FT NON_TER 133
SQ SEQUENCE 133 AA; 15775 MW; 8DED10B25057F953 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 133;
Best Local Similarity 96.2%; Pred. No. 2.1e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLLGWCSGKLC 26
   |:|||||
Db 36 RVLAVERYLKDQQLLGWCSGKLC 61
   |:|||||

RESULT 237
Q8UQ24 PRELIMINARY; PRT; 133 AA.
AC Q8UQ24;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=98ZM043N;
RX MEDLINE=21602569; PubMed=11739704;
RA Traak S.A., Derdeyn C.A., Fidelity U., Chen Y., Meleth S., Kasolo F.,
RA Musonda R., Hunter E., Gao F., Allen S., Hahn B.H.;
RT "Molecular epidemiology of human immunodeficiency virus type 1
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RT transmission in a heterosexual cohort of discordant couples in
RT Zambia.";
RT J. Virol. 76:397-405(2002).
DR EMBL; AF405154; AAL66674.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 133
FT NON_TER 133
SQ SEQUENCE 133 AA; 16057 MW; 6650DBE2480703B0 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 133;
Best Local Similarity 96.2%; Pred. No. 2.1e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLLGWCSGKLC 26
   |:|||||
Db 27 RVLAVERYLKDQQLLGWCSGKLC 52
   |:|||||

RESULT 238
Q90Q25 PRELIMINARY; PRT; 133 AA.
AC Q90Q25;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=99ES-MO1541;
RX MEDLINE=21322034; PubMed=11429126;
RA Ortiz M., Sanchez I., Gonzalez M.P., Leon M.I., Abeso N., Asumu E.,
RA Garcia-Saiz A.;
RT "Molecular epidemiology of HIV type 1 subtypes in Equatorial Guinea.";
RL AIDS Res. Hum. Retroviruses 17:851-855(2001).
DR EMBL; AF331116; AAK92327.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 133
FT NON_TER 133
SQ SEQUENCE 133 AA; 15821 MW; D62443B42FE9EA93 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 133;
Best Local Similarity 96.2%; Pred. No. 2.1e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLLGWCSGKLC 26
   |:|||||
Db 36 RVLAVERYLKDQQLLGWCSGKLC 61
   |:|||||

RESULT 239
Q8UQ23 PRELIMINARY; PRT; 133 AA.
AC Q8UQ23;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
```

```
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=97ZM043F;
RX MEDLINE=21602569; PubMed=11739704;
RA Trask S.A., Derdeyn C.A., Fideli U., Chen Y., Meleth S., Kasolo F.,
RA Musonda R., Hunter E., Gao F., Allen S., Hahn B.H.;
RT "Molecular epidemiology of human immunodeficiency virus type 1
RT transmission in a heterosexual cohort of discordant couples in
RT Zambia."; 76:397-405(2002).
RL J. Virol. 76:397-405(2002).
DR EMBL; AF405155; AAL66675.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON TER 1
FT NON TER 133
SQ SEQUENCE 133 AA; 16058 MW; 665E360246E9E3B0 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 133;
Best Local Similarity 96.2%; Pred. No. 2.1e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RILAVERYLKDQQLGIWGCGSKLIC 26
|:|||||
Db 27 RVLAVERYLKDQQLGIWGCGSKLIC 52
|:|||||

RESULT 240
Q9IWR3 PRELIMINARY; PRT; 133 AA.
AC Q9IWR3
DT 01-OCT-2000 (TREMELrel. 15, Created)
DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=85CD300;
RX MEDLINE=21134754; PubMed=11242522;
RA Yang C., Dash B., Hanna S.L., Frances H.S., Nzilambi N.,
RA Colebunders R.C., St Louis M., Quinn T.C., Folks T.M., Lal R.B.;
RT "Predominance of HIV type 1 subtype G among commercial sex workers
RT from Kinshasa, Democratic Republic of Congo.";
RL AIDS Res. Hum. Retroviruses 17:361-365(2001).
DR EMBL; AF260463; AAF71930.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON TER 1
FT NON TER 133
SQ SEQUENCE 133 AA; 16036 MW; 60554BC9396A823 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 133;
Best Local Similarity 96.2%; Pred. No. 2.1e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RILAVERYLKDQQLGIWGCGSKLIC 26
|:|||||
Db 24 RILAVERYLKDQQLGIWGCGSKLIC 49
|:|||||

RESULT 241
Q9OQ27 PRELIMINARY; PRT; 133 AA.
AC Q9OQ27
DT 01-DEC-2001 (TREMELrel. 19, Created)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=99ES-MO1536;
RX MEDLINE=21322034; PubMed=11429126;
RA Ortiz M., Sanchez I., Gonzalez M.P., Leon M.I., Abeso N., Asumu E.,
RA Garcia-Saiz A.;
RT "Molecular epidemiology of HIV type 1 subtypes in Equatorial Guinea.";
RL AIDS Res. Hum. Retroviruses 17:851-855(2001).
DR EMBL; AF331114; AAK92325.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON TER 1
FT NON TER 133
SQ SEQUENCE 133 AA; 15658 MW; 200E08E3482A65A CRC64;

Query Match 99.3%; Score 138; DB 15; Length 133;
Best Local Similarity 96.2%; Pred. No. 2.1e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RILAVERYLKDQQLGIWGCGSKLIC 26
|:|||||
Db 36 RVLAVERYLKDQQLGIWGCGSKLIC 61
|:|||||

RESULT 242
Q9OQ35 PRELIMINARY; PRT; 133 AA.
AC Q9OQ35
DT 01-DEC-2001 (TREMELrel. 19, Created)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=99ES-MO1521;
RX MEDLINE=21322034; PubMed=11429126;
RA Ortiz M., Sanchez I., Gonzalez M.P., Leon M.I., Abeso N., Asumu E.,
RA Garcia-Saiz A.;
RT "Molecular epidemiology of HIV type 1 subtypes in Equatorial Guinea.";
RL AIDS Res. Hum. Retroviruses 17:851-855(2001).
DR EMBL; AF331106; AAK92317.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON TER 1
FT NON TER 133
SQ SEQUENCE 133 AA; 15794 MW; 9426B9B28EA26F6F CRC64;

Query Match 99.3%; Score 138; DB 15; Length 133;
Best Local Similarity 96.2%; Pred. No. 2.1e-13;
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Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 RILAVERYLKDQQLLGWCSGKLC 26
Db 36 RVLAVERYLKDQQLLGWCSGKLC 61

RESULT 243
Q9IWQ6 PRELIMINARY; PRT; 134 AA.
AC Q9IWQ6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=85CD260;
RX MEDLINE=21134754; PubMed=11242522;
RA Yang C., Dash B., Hanna S.L., Frances H.S., Nzilambi N.,
RA Colebunders R.C., St Louis M., Quinn T.C., Folks T.M., Lal R.B.;
RT "Predominance of HIV type 1 subtype G among commercial sex workers
RT from Kinshasa, Democratic Republic of Congo.";
RL AIDS Res. Hum. Retroviruses 17:361-365(2001).
DR EMBL; AF260470; RAF1937.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1 1
FT NON_TER 134 134
SQ SEQUENCE 134 AA; 15361 MW; EA6E5DFE360A0322 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 134;
Best Local Similarity 96.2%; Pred. No. 2.1e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 RILAVERYLKDQQLLGWCSGKLC 26
Db 34 RVLAVERYLKDQQLLGWCSGKLC 59

RESULT 244
Q8UQZ5 PRELIMINARY; PRT; 136 AA.
AC Q8UQZ5;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=00ZM148M;
RX MEDLINE=21602569; PubMed=11739704;
RA Trask S.A., Derynck C.A., Fidelis U., Chen Y., Meleth S., Kasolo F.,
RA Musonda R., Hunter E., Gao F., Allen S., Hahn B.H.;
RT "Molecular epidemiology of human immunodeficiency virus type 1
RT transmission in a heterosexual cohort of discordant couples in
RT Zambia.";
RL J. Virol. 76:397-405(2002).
DR EMBL; AF405153; AAL66673.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
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DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1 1
FT NON_TER 136 136
SQ SEQUENCE 136 AA; 16415 MW; EF1069F332CF8128 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 136;
Best Local Similarity 96.2%; Pred. No. 2.2e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 RILAVERYLKDQQLLGWCSGKLC 26
Db 24 RVLAVERYLKDQQLLGWCSGKLC 49

RESULT 245
Q9DQMO PRELIMINARY; PRT; 137 AA.
AC Q9DQMO;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SP-M1270;
RX MEDLINE=20584646; PubMed=11153079;
RA Ortiz M., Munoz L., Bernal A., Rodriguez A., Zorraquino A.,
RA Vellido J., Salas A., Moreno A., Garcia-Saiz A.;
RT "Molecular Characterization of Non-B HIV Type 1 Subtypes from Africa
RT in Spain.";
RL AIDS Res. Hum. Retroviruses 16:1967-1971(2000).
DR EMBL; AF255938; AAG36893.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1 1
FT NON_TER 137 137
SQ SEQUENCE 137 AA; 16458 MW; 94CED7A1B23984C1 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 137;
Best Local Similarity 96.2%; Pred. No. 2.2e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 RILAVERYLKDQQLLGWCSGKLC 26
Db 35 RVLAVERYLKDQQLLGWCSGKLC 60

RESULT 246
Q7SLZ5 PRELIMINARY; PRT; 139 AA.
AC Q7SLZ5;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GT853;
```

RA Gonzalez Perez M.P., Garcia Saiz A.;
RT "Epidemiological and molecular characteristics of HIV and HTLV
infection in Equatorial Guinea, 1996-1998.";
RL Submitted (JUL-2002) to the ENBL/GenBank/DBJ databases.
DR EMBL; AF530021; AAP87732.1; -
KW Envelope protein.
FT NON TER 1
FT NON TER 139 139
SQ SEQUENCE 139 AA; 16799 MW; C94B96DEB9658C CRC64;

Query Match 99.3%; Score 138; DB 15; Length 139;
Best Local Similarity 96.2%; Pred. No. 2.2e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSKGLIC 26
|:|||||
Db 37 RVLAVERYLKDQQLGIWCGSKGLIC 62

RESULT 247

Q7SM28
ID Q7SM28 PRELIMINARY; PRT; 140 AA.
AC Q7SM28;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GM577;
RA Gonzalez Perez M.P., Garcia Saiz A.;
RT "Epidemiological and molecular characteristics of HIV and HTLV
infection in Equatorial Guinea, 1996-1998.";
RL Submitted (JUL-2002) to the ENBL/GenBank/DBJ databases.
DR EMBL; AF529988; AAP87719.1; -
KW Envelope protein.
FT NON TER 1
FT NON TER 140 140
SQ SEQUENCE 140 AA; 16660 MW; 4864908A23F36A6A CRC64;

Query Match 99.3%; Score 138; DB 15; Length 140;
Best Local Similarity 96.2%; Pred. No. 2.2e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSKGLIC 26
|:|||||
Db 37 RVLAVERYLKDQQLGIWCGSKGLIC 62

RESULT 248

Q9IWQ1
ID Q9IWQ1 PRELIMINARY; PRT; 143 AA.
AC Q9IWQ1;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=85CD350;
RX MEDLINE=21134754; PubMed=11242522;
RA Yang C., Dash B., Hanna S.L., Frances H.S., Nzilambi N.,
Colebunders R.C., Quinn T.C., Folks T.M., Lal R.B.;
RT "Predominance of HIV type 1 subtype G among commercial sex workers
from Kinshasa, Democratic Republic of Congo.";

RL AIDS Res. Hum. Retroviruses 17:361-365(2001).
DR EMBL; AF260475; AAF71942.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; F:structural molecule activity; IEA.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON TER 1
FT NON TER 143 143
SQ SEQUENCE 143 AA; 17160 MW; D8157A905740B24E CRC64;

Query Match 99.3%; Score 138; DB 15; Length 143;
Best Local Similarity 96.2%; Pred. No. 2.3e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSKGLIC 26
|:|||||
Db 35 RVLAVERYLKDQQLGIWCGSKGLIC 60

RESULT 249

Q9IWP3
ID Q9IWP3 PRELIMINARY; PRT; 144 AA.
AC Q9IWP3;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=85CD299;
RX MEDLINE=21134754; PubMed=11242522;
RA Yang C., Dash B., Hanna S.L., Frances H.S., Nzilambi N.,
Colebunders R.C., Quinn T.C., Folks T.M., Lal R.B.;
RT "Predominance of HIV type 1 subtype G among commercial sex workers
from Kinshasa, Democratic Republic of Congo.";
RL AIDS Res. Hum. Retroviruses 17:361-365(2001).
DR EMBL; AF260483; AAF71950.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON TER 1
FT NON TER 144 144
SQ SEQUENCE 144 AA; 17098 MW; 2D21BB1C3390CC29 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 144;
Best Local Similarity 96.2%; Pred. No. 2.3e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSKGLIC 26
|:|||||
Db 35 RVLAVERYLKDQQLGIWCGSKGLIC 60

RESULT 250

Q70207
ID Q70207 PRELIMINARY; PRT; 144 AA.
AC Q70207;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Envelope glycoprotein gp41 region (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

```

OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PBLPD;
RX MEDLINE=95251923; PubMed=7734184;
RA Calabro M.L., Zanotto C., Calderazzo F., Crivellaro C., Del Mistro A.,
RA De Rossi A., Chieco-Bianchi L.;
RT "HIV-1 infection of the thymus: evidence for a cytopathic and
RT thymotropic viral variant in vivo.";
RL AIDS Res. Hum. Retroviruses 11:11-19(1995).
DR EMBL; U09253; AAA79038.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 144
SQ SEQUENCE 144 AA; 17229 MW; 4B2F7347B3E65C4A CRC64;

Query Match 99.3%; Score 138; DB 15; Length 144;
Best Local Similarity 96.2%; Pred. No. 2.3e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 R1LAVERYLKDQQLGWCSCGKLC 26
DB 34 RVLAVERYLKDQQLGWCSCGKLC 59

RESULT 251
Q70206 ID Q70206 PRELIMINARY; PRT; 144 AA.
AC Q70206;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein gp41 region (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=THYPD;
RX MEDLINE=95251923; PubMed=7734184;
RA Calabro M.L., Zanotto C., Calderazzo F., Crivellaro C., Del Mistro A.,
RA De Rossi A., Chieco-Bianchi L.;
RT "HIV-1 infection of the thymus: evidence for a cytopathic and
RT thymotropic viral variant in vivo.";
RL AIDS Res. Hum. Retroviruses 11:11-19(1995).
DR EMBL; U09252; AAA79038.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 144
SQ SEQUENCE 144 AA; 17227 MW; 233F7297E0E12C5B CRC64;

Query Match 99.3%; Score 138; DB 15; Length 144;
Best Local Similarity 96.2%; Pred. No. 2.3e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 R1LAVERYLKDQQLGWCSCGKLC 26
DB 34 RVLAVERYLKDQQLGWCSCGKLC 59

RESULT 252
Q7ZCE9 ID Q7ZCE9 PRELIMINARY; PRT; 144 AA.
AC Q7ZCE9;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HRLUX50-1;
RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,
RA Staub T., Bouleme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;
RT "Uncommon mutations at residue positions critical for enfuvirtide (T-
RT 20) resistance in enfuvirtide-naive patients infected with subtype B
RT and non-B HIV-1.";
RL Submitted (NOV-2002) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AY185378; AAO65653.1; -.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Envelope protein.
FT NON_TER 1
FT NON_TER 144
SQ SEQUENCE 144 AA; 16770 MW; C3A3781F5BF13207 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 144;
Best Local Similarity 96.2%; Pred. No. 2.3e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 R1LAVERYLKDQQLGWCSCGKLC 26
DB 50 RVLAVERYLKDQQLGWCSCGKLC 75

RESULT 253
Q7ZCE2 ID Q7ZCE2 PRELIMINARY; PRT; 144 AA.
AC Q7ZCE2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HRLUX50-1;
RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,
RA Staub T., Bouleme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;
RT "Uncommon mutations at residue positions critical for enfuvirtide (T-
RT 20) resistance in enfuvirtide-naive patients infected with subtype B
RT and non-B HIV-1.";
RL Submitted (NOV-2002) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AY185378; AAO65653.1; -.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Envelope protein.
FT NON_TER 1
FT NON_TER 144
SQ SEQUENCE 144 AA; 16770 MW; C3A3781F5BF13207 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 144;
Best Local Similarity 96.2%; Pred. No. 2.3e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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```
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]_TaxID=11676;
RC STRAIN=HRLUX63-2;
RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,
RA Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;
RT "Uncommon mutations at residue positions critical for enfuvirtide (T-
RT 20) resistance in enfuvirtide-naïve patients infected with subtype B
RT and non-B HIV-1.";
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY185402; AAO65677.1; -.
DR GO; GO:0019031; C:viral envelope; IEA.
DR InterPro; IPR000328; F:structural molecule activity; IEA.
DR Pfam; PF00517; GP41; 1.
KW Envelope protein.
FT NON_TER 1
FT NON_TER 144
SQ SEQUENCE 144 AA; 16951 MW; 99940DA637DA9D7F CRC64;

Query Match 99.3%; Score 138; DB 15; Length 144;
Best Local Similarity 96.2%; Pred. No. 2.3e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCCKLIC 26
Db 50 RVLAVERYLKDQQLGIWGCCKLIC 75

RESULT 262
Q7ZCB5 ID Q7ZCB5 PRELIMINARY; PRT; 144 AA.
AC Q7ZCB5;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]_TaxID=11676;
RC STRAIN=HRLUX65-1;
RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,
RA Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;
RT "Uncommon mutations at residue positions critical for enfuvirtide (T-
RT 20) resistance in enfuvirtide-naïve patients infected with subtype B
RT and non-B HIV-1.";
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY185405; AAO65680.1; -.
DR GO; GO:0019031; C:viral envelope; IEA.
DR InterPro; IPR000328; F:structural molecule activity; IEA.
DR Pfam; PF00517; GP41; 1.
KW Envelope protein.
FT NON_TER 1
FT NON_TER 144
SQ SEQUENCE 144 AA; 16937 MW; 68F2D1D36DBF781B CRC64;

Query Match 99.3%; Score 138; DB 15; Length 144;
Best Local Similarity 96.2%; Pred. No. 2.3e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCCKLIC 26
Db 50 RVLAVERYLKDQQLGIWGCCKLIC 75

RESULT 263
Q7ZCB4 ID Q7ZCB4 PRELIMINARY; PRT; 144 AA.
AC Q7ZCB4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]_TaxID=11676;
RC STRAIN=HRLUX65-2;
RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,
RA Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;
RT "Uncommon mutations at residue positions critical for enfuvirtide (T-
RT 20) resistance in enfuvirtide-naïve patients infected with subtype B
RT and non-B HIV-1.";
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY185406; AAO65681.1; -.
DR GO; GO:0019031; C:viral envelope; IEA.
DR InterPro; IPR000328; F:structural molecule activity; IEA.
DR Pfam; PF00517; GP41; 1.
KW Envelope protein.
FT NON_TER 1
FT NON_TER 144
SQ SEQUENCE 144 AA; 16938 MW; 68FF6ABED6DF781B CRC64;

Query Match 99.3%; Score 138; DB 15; Length 144;
Best Local Similarity 96.2%; Pred. No. 2.3e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCCKLIC 26
Db 50 RVLAVERYLKDQQLGIWGCCKLIC 75

RESULT 264
Q7ZCB1 ID Q7ZCB1 PRELIMINARY; PRT; 144 AA.
AC Q7ZCB1;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]_TaxID=11676;
RC STRAIN=HRLUX67-1;
RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,
RA Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;
RT "Uncommon mutations at residue positions critical for enfuvirtide (T-
RT 20) resistance in enfuvirtide-naïve patients infected with subtype B
RT and non-B HIV-1.";
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY185409; AAO65684.1; -.
DR GO; GO:0019031; C:viral envelope; IEA.
DR InterPro; IPR000328; F:structural molecule activity; IEA.
DR Pfam; PF00517; GP41; 1.
KW Envelope protein.
FT NON_TER 1
FT NON_TER 144
SQ SEQUENCE 144 AA; 16904 MW; C4E289C330AA4F41 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 144;
Best Local Similarity 96.2%; Pred. No. 2.3e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCCKLIC 26
Db 50 RVLAVERYLKDQQLGIWGCCKLIC 75
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Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGWSGKGLIC 26
FT NON_TER 144
SQ SEQUENCE 144 AA; 16701 MW; 40FFFCF6BBF14F4 CRC64;
Db 50 RVLAVERYLKDQQLGWSGKGLIC 75

RESULT 265

Q7ZCB0
ID Q7ZCB0 PRELIMINARY; PRT; 144 AA.

AC Q7ZCB0; 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.

OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;

RN [1]

RC STRAIN=HRLUX67-2;

RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,
Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;
"Uncommon mutations at residue positions critical for enfuvirtide (T-
20) resistance in enfuvirtide-naive patients infected with subtype B
RT and non-B HIV-1.";
RT Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL; AV185410; AAO65685.1; --

DR GO; GO:0019031; C:Viral envelope; IEA.

DR GO; GO:0005198; F:Structural molecule activity; IEA.

DR InterPro; IPR000328; Env_GP41.

DR Pfam; PF00517; GP41; 1.

KW Envelope protein.

FT NON_TER 1

FT NON_TER 144

SQ SEQUENCE 144 AA; 16904 MW; C4E289C330AA4F41 CRC64;
Query Match 99.3%; Score 138; DB 15; Length 144;
Best Local Similarity 96.2%; Pred. No. 2.3e-13;

Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGWSGKGLIC 26
FT NON_TER 144
SQ SEQUENCE 144 AA; 16706 MW; 10D841FB587B9ECC CRC64;
Db 50 RVLAVERYLKDQQLGWSGKGLIC 75

RESULT 266

Q7ZCA6
ID Q7ZCA6 PRELIMINARY; PRT; 144 AA.

AC Q7ZCA6; 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.

OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;

RN [1]

RC STRAIN=HRLUX70-1;

RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,
Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;
"Uncommon mutations at residue positions critical for enfuvirtide (T-
20) resistance in enfuvirtide-naive patients infected with subtype B
RT and non-B HIV-1.";
RT Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL; AV185414; AAO65689.1; --

DR GO; GO:0019031; C:Viral envelope; IEA.

DR GO; GO:0005198; F:Structural molecule activity; IEA.

DR InterPro; IPR000328; Env_GP41.

DR Pfam; PF00517; GP41; 1.

KW Envelope protein.

FT NON_TER 1

FT NON_TER 144

SQ SEQUENCE 144 AA; 16706 MW; 10D841FB587B9ECC CRC64;
Query Match 99.3%; Score 138; DB 15; Length 144;
Best Local Similarity 96.2%; Pred. No. 2.3e-13;

Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

KW Envelope protein.

FT NON_TER 1

FT NON_TER 144

SQ SEQUENCE 144 AA; 16701 MW; 40FFFCF6BBF14F4 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 144;

Best Local Similarity 96.2%; Pred. No. 2.3e-13;

Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGWSGKGLIC 26

FT NON_TER 144

SQ SEQUENCE 144 AA; 16701 MW; 40FFFCF6BBF14F4 CRC64;

RESULT 267

Q7ZCA5

ID Q7ZCA5 PRELIMINARY; PRT; 144 AA.

AC Q7ZCA5;

DT 01-JUN-2003 (TrEMBLrel. 24, Created)

DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Envelope glycoprotein (Fragment).

GN ENV.

OS Human immunodeficiency virus 1.

OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.

OX NCBI_TaxID=11676;

RN [1]

RC STRAIN=HRLUX70-2;

RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,
Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;
"Uncommon mutations at residue positions critical for enfuvirtide (T-
20) resistance in enfuvirtide-naive patients infected with subtype B
RT and non-B HIV-1.";
RT Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL; AV185415; AAO65690.1; --

DR GO; GO:0019031; C:Viral envelope; IEA.

DR GO; GO:0005198; F:Structural molecule activity; IEA.

DR InterPro; IPR000328; Env_GP41.

DR Pfam; PF00517; GP41; 1.

KW Envelope protein.

FT NON_TER 1

FT NON_TER 144

SQ SEQUENCE 144 AA; 16706 MW; 10D841FB587B9ECC CRC64;
Query Match 99.3%; Score 138; DB 15; Length 144;
Best Local Similarity 96.2%; Pred. No. 2.3e-13;

Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGWSGKGLIC 26

FT NON_TER 144

SQ SEQUENCE 144 AA; 16706 MW; 10D841FB587B9ECC CRC64;

Query Match 99.3%; Score 138; DB 15; Length 144;

Best Local Similarity 96.2%; Pred. No. 2.3e-13;

Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 268

Q7ZC98

ID Q7ZC98 PRELIMINARY; PRT; 144 AA.

AC Q7ZC98;

DT 01-JUN-2003 (TrEMBLrel. 24, Created)

DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Envelope glycoprotein (Fragment).

GN ENV.

OS Human immunodeficiency virus 1.

OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.

OX NCBI_TaxID=11676;

RN [1]

RC STRAIN=HRLUX74-1;

RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,
Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;
"Uncommon mutations at residue positions critical for enfuvirtide (T-
20) resistance in enfuvirtide-naive patients infected with subtype B
RT and non-B HIV-1.";
RT Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL; AV185414; AAO65689.1; --

DR GO; GO:0019031; C:Viral envelope; IEA.

DR GO; GO:0005198; F:Structural molecule activity; IEA.

DR InterPro; IPR000328; Env_GP41.

DR Pfam; PF00517; GP41; 1.

KW Envelope protein.

FT NON_TER 1

FT NON_TER 144

SQ SEQUENCE 144 AA; 16706 MW; 10D841FB587B9ECC CRC64;
Query Match 99.3%; Score 138; DB 15; Length 144;
Best Local Similarity 96.2%; Pred. No. 2.3e-13;

Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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RT and non-B HIV-1."
RL Submitted (NOV-2002) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AY185422; AAO65697.1; -.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Envelope protein.
FT NON TER 1
FT NON TER 144
SQ SEQUENCE 144 AA; 16833 MW; 0FB4031FCB7D4BCE CRC64;

Query Match 99.3%; Score 138; DB 15; Length 144;
Best Local Similarity 96.2%; Pred. No. 2.3e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSGKLC 26
DB 50 RVLAVERYLKDQQLGIWCGSGKLC 75

RESULT 269
Q7ZC96 PRELIMINARY; PRT; 144 AA.
AC Q7ZC96;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein (Fragment).
ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrod viruses; Retroviridae; Lentivirus.
ON NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,
RA Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;
RT "Uncommon mutations at residue positions critical for enfuvirtide (T-
RT 20) resistance in enfuvirtide-naive patients infected with subtype B
RT and non-B HIV-1."
RL Submitted (NOV-2002) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AY185424; AAO65699.1; -.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Envelope protein.
FT NON TER 1
FT NON TER 144
SQ SEQUENCE 144 AA; 16877 MW; 619841A2A7D5ECD4 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 144;
Best Local Similarity 96.2%; Pred. No. 2.3e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSGKLC 26
DB 50 RVLAVERYLKDQQLGIWCGSGKLC 75

RESULT 270
Q7ZC95 PRELIMINARY; PRT; 144 AA.
AC Q7ZC95;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein (Fragment).
ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrod viruses; Retroviridae; Lentivirus.
ON NCBI_TaxID=11676;
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RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HRLUX75-2;
RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,
RA Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;
RT "Uncommon mutations at residue positions critical for enfuvirtide (T-
RT 20) resistance in enfuvirtide-naive patients infected with subtype B
RT and non-B HIV-1."
RL Submitted (NOV-2002) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AY185425; AAO65700.1; -.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Envelope protein.
FT NON TER 1
FT NON TER 144
SQ SEQUENCE 144 AA; 16856 MW; E89941A2A9E2F16C CRC64;

Query Match 99.3%; Score 138; DB 15; Length 144;
Best Local Similarity 96.2%; Pred. No. 2.3e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSGKLC 26
DB 50 RVLAVERYLKDQQLGIWCGSGKLC 75

RESULT 271
Q7ZC71 PRELIMINARY; PRT; 144 AA.
AC Q7ZC71;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein (Fragment).
ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrod viruses; Retroviridae; Lentivirus.
ON NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HRLUX89-1;
RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,
RA Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;
RT "Uncommon mutations at residue positions critical for enfuvirtide (T-
RT 20) resistance in enfuvirtide-naive patients infected with subtype B
RT and non-B HIV-1."
RL Submitted (NOV-2002) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AY185449; AAO65724.1; -.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Envelope protein.
FT NON TER 1
FT NON TER 144
SQ SEQUENCE 144 AA; 16824 MW; F1EBA0FCC4691895 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 144;
Best Local Similarity 96.2%; Pred. No. 2.3e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSGKLC 26
DB 50 RVLAVERYLKDQQLGIWCGSGKLC 75

RESULT 272
Q7ZC70 PRELIMINARY; PRT; 144 AA.
AC Q7ZC70;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
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DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HRLUX89-2;
RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,
RA Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;
RT "Uncommon mutations at residue positions critical for enfuvirtide (T-
RT 20) resistance in enfuvirtide-naive patients infected with subtype B
RT and non-B HIV-1."
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY185450; AAO65725.1; -.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Envelope protein.
FT NON_TER 1 1
FT NON_TER 144 144
SQ SEQUENCE 144 AA; 16810 MW; E811A60B17491895 CRC64;

Query Match          99.3%; Score 138; DB 15; Length 144;
Best Local Similarity 96.2%; Pred. No. 2.3e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGICSGKLC 26
DB 50 RVLAVERYLKDQQLGICSGKLC 75

RESULT 273
QY 07ZC66 PRELIMINARY; PRT; 145 AA.
AC 07ZC66;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HRLUX4;
RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,
RA Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;
RT "Uncommon mutations at residue positions critical for enfuvirtide (T-
RT 20) resistance in enfuvirtide-naive patients infected with B and non-B
RT subtype HIV-1."
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY185454; AAO65729.1; -.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Envelope protein.
FT NON_TER 1 1
FT NON_TER 145 145
SQ SEQUENCE 145 AA; 16911 MW; AF6C707A2076B6DE CRC64;

Query Match          99.3%; Score 138; DB 15; Length 145;
Best Local Similarity 96.2%; Pred. No. 2.3e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGICSGKLC 26
DB 48 RVLAVERYLKDQQLGICSGKLC 73

RESULT 274
QY 07ZC49 PRELIMINARY; PRT; 145 AA.
AC 07ZC49;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HRLUX21;
RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,
RA Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;
RT "Uncommon mutations at residue positions critical for enfuvirtide (T-
RT 20) resistance in enfuvirtide-naive patients infected with B and non-B
RT subtype HIV-1."
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY185471; AAO65746.1; -.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Envelope protein.
FT NON_TER 1 1
FT NON_TER 145 145
SQ SEQUENCE 145 AA; 17036 MW; FA30B782F065B72D CRC64;

Query Match          99.3%; Score 138; DB 15; Length 145;
Best Local Similarity 96.2%; Pred. No. 2.3e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGICSGKLC 26
DB 48 RVLAVERYLKDQQLGICSGKLC 73

RESULT 275
QY 07ZC39 PRELIMINARY; PRT; 145 AA.
AC 07ZC39;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HRLUX31;
RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,
RA Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;
RT "Uncommon mutations at residue positions critical for enfuvirtide (T-
RT 20) resistance in enfuvirtide-naive patients infected with B and non-B
RT subtype HIV-1."
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY185481; AAO65756.1; -.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Envelope protein.
FT NON_TER 1 1
FT NON_TER 145 145
SQ SEQUENCE 145 AA; 17033 MW; F899F94713F5D4D0 CRC64;
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Query Match 99.3%; Score 138; DB 15; Length 145;
Best Local Similarity 96.2%; Pred. No. 2.3e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLLGWCGSKLIC 26
|:|||||
Db 48 RVLAVERYLKDQQLLGWCGSKLIC 73

RESULT 276

Q7ZC33 ID Q7ZC33 PRELIMINARY; PRT; 145 AA.
AC Q7ZC33;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
[1]
RC STRAIN=HRLUX37;
RP SEQUENCE FROM N.A.
RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,
RA Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;
RT "Uncommon mutations at residue positions critical for enfuvirtide (T-
RT 20) resistance in enfuvirtide-naive patients infected with B and non-B
RT subtype HIV-1.";
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY185487; AA065762.1; -;
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Envelope protein.
FT NON_TER 1
FT NON_TER 145
SQ SEQUENCE 145 AA; 16912 MW; F4BFB6175BD662D CRC64;

Query Match 99.3%; Score 138; DB 15; Length 145;
Best Local Similarity 96.2%; Pred. No. 2.3e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLLGWCGSKLIC 26
|:|||||
Db 48 RVLAVERYLKDQQLLGWCGSKLIC 73

RESULT 277

Q7ZC32 ID Q7ZC32 PRELIMINARY; PRT; 145 AA.
AC Q7ZC32;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
[1]
RC STRAIN=HRLUX38;
RP SEQUENCE FROM N.A.
RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,
RA Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;
RT "Uncommon mutations at residue positions critical for enfuvirtide (T-
RT 20) resistance in enfuvirtide-naive patients infected with B and non-B
RT subtype HIV-1.";
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY185488; AA065763.1; -;
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.

DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Envelope protein.
FT NON_TER 1
FT NON_TER 145
SQ SEQUENCE 145 AA; 17043 MW; 4487A149CEC57570 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 145;
Best Local Similarity 96.2%; Pred. No. 2.3e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLLGWCGSKLIC 26
|:|||||
Db 48 RVLAVERYLKDQQLLGWCGSKLIC 73

RESULT 278

Q7ZC68 ID Q7ZC68 PRELIMINARY; PRT; 146 AA.
AC Q7ZC68;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
[1]
RC STRAIN=HRLUX2;
RP SEQUENCE FROM N.A.
RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,
RA Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;
RT "Uncommon mutations at residue positions critical for enfuvirtide (T-
RT 20) resistance in enfuvirtide-naive patients infected with B and non-B
RT subtype HIV-1.";
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY185452; AA065727.1; -;
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Envelope protein.
FT NON_TER 1
FT NON_TER 146
SQ SEQUENCE 146 AA; 17151 MW; 70D3C7B584C9DA3A CRC64;

Query Match 99.3%; Score 138; DB 15; Length 146;
Best Local Similarity 96.2%; Pred. No. 2.3e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLLGWCGSKLIC 26
|:|||||
Db 48 RVLAVERYLKDQQLLGWCGSKLIC 73

RESULT 279

Q7ZC30 ID Q7ZC30 PRELIMINARY; PRT; 146 AA.
AC Q7ZC30;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
[1]
RC STRAIN=HRLUX40;
RP SEQUENCE FROM N.A.
RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,
RA Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;


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RA Boutonnet N., Janssens W., Boutton C., Verschelde J.L., Heyndrickx L.,
RA Beirnaert E., van der Groen G., Lasters I.;
RT "Comparison of predicted scaffold-compatible sequence variation in the
RT triple-hairpin structure of human immunodeficiency virus type 1 gp41
RT with patient data.";
RL J. Virol. 76:7595-7606(2002).
DR EMBL; AJ428002; CAD20954.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 155
SQ SEQUENCE 155 AA; 18273 MW; B4EBAC6F0C278B2F CRC64;

Query Match 99.3%; Score 138; DB 15; Length 155;
Best Local Similarity 96.2%; Pred. No. 2.5e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RILAVERYLKDQQLGIWGCGSKLIC 26
|:|||||
Db 35 RVLAVERYLKDQQLGIWGCGSKLIC 60

RESULT 284
Q8JAL7 PRELIMINARY; PRT; 156 AA.
AC Q8JAL7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=95BRJ014;
RA Guimaraes M.L., Moreira A.S., Loureiro R., Galvao-Castro B.,
RA Morgado M.G.;
RT "High frequency of recombinant genomes in HIV-1 samples from Brazilian
RT Southeastern and Southern regions.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF463427; AAM90803.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 156
SQ SEQUENCE 156 AA; 17855 MW; 21F22059FB9A919B CRC64;

Query Match 99.3%; Score 138; DB 15; Length 156;
Best Local Similarity 96.2%; Pred. No. 2.5e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RILAVERYLKDQQLGIWGCGSKLIC 26
|:|||||
Db 55 RVLAVERYLKDQQLGIWGCGSKLIC 80

RESULT 285
Q8U3Q9 PRELIMINARY; PRT; 156 AA.
AC Q8U3Q9;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp41 protein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=95BRJ014;
RA Guimaraes M.L., Moreira A.S., Loureiro R., Galvao-Castro B.,
RA Morgado M.G.;
RT "High frequency of recombinant genomes in HIV-1 samples from Brazilian
RT Southeastern and Southern regions.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF463427; AAM90803.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 156
SQ SEQUENCE 156 AA; 17855 MW; 21F22059FB9A919B CRC64;

Query Match 99.3%; Score 138; DB 15; Length 156;
Best Local Similarity 96.2%; Pred. No. 2.5e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RILAVERYLKDQQLGIWGCGSKLIC 26
|:|||||
Db 55 RVLAVERYLKDQQLGIWGCGSKLIC 80

RESULT 286
Q90E80 PRELIMINARY; PRT; 163 AA.
AC Q90E80;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SC15;
RA Feng H., Huang Y., Yang D., Tang H., Hu X.;
RA "Phylogenetic analysis of part of env gene of HIV-1 isolates from
RA Sichuan.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY037950; AAK72323.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 163
SQ SEQUENCE 163 AA; 19242 MW; C580C6B44534772E CRC64;

Query Match 99.3%; Score 138; DB 15; Length 163;
Best Local Similarity 96.2%; Pred. No. 2.6e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RILAVERYLKDQQLGIWGCGSKLIC 26
|:|||||
Db 51 RVLAVERYLKDQQLGIWGCGSKLIC 76

RESULT 287
Q90E76
```

```
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22092513; PubMed=12097573;
RA Boutonnet N., Janssens W., Boutton C., Verschelde J.L., Heyndrickx L.,
RA Beirnaert E., van der Groen G., Lasters I.;
RT "Comparison of predicted scaffold-compatible sequence variation in the
RT triple-hairpin structure of human immunodeficiency virus type 1 gp41
RT with patient data.";
RL J. Virol. 76:7595-7606(2002).
DR EMBL; AJ427994; CAD20946.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 156
SQ SEQUENCE 156 AA; 18491 MW; 54BFB80BC6FB76DD CRC64;

Query Match 99.3%; Score 138; DB 15; Length 156;
Best Local Similarity 96.2%; Pred. No. 2.5e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RILAVERYLKDQQLGIWGCGSKLIC 26
|:|||||
Db 35 RVLAVERYLKDQQLGIWGCGSKLIC 60

RESULT 286
Q90E80 PRELIMINARY; PRT; 163 AA.
AC Q90E80;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SC15;
RA Feng H., Huang Y., Yang D., Tang H., Hu X.;
RA "Phylogenetic analysis of part of env gene of HIV-1 isolates from
RA Sichuan.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY037950; AAK72323.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 163
SQ SEQUENCE 163 AA; 19242 MW; C580C6B44534772E CRC64;

Query Match 99.3%; Score 138; DB 15; Length 163;
Best Local Similarity 96.2%; Pred. No. 2.6e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RILAVERYLKDQQLGIWGCGSKLIC 26
|:|||||
Db 51 RVLAVERYLKDQQLGIWGCGSKLIC 76

RESULT 287
Q90E76
```


ID Q90E76 PRELIMINARY; PRT; 163 AA.
AC Q90E76;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SC27;
RA Feng H., Huang Y., Yang D., Tang H., Hu X.;
RT "Phylogenetic analysis of part of env gene of HIV-1 isolates from Sichuan."
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY037954; AAK72327.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 163
SQ SEQUENCE 163 AA; 19285 MW; 28991707613DIFE CRC64;

Query Match 99.3%; Score 138; DB 15; Length 163;
Best Local Similarity 96.2%; Pred. No. 2.6e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIGCGSKLIC 26
|:|||||||||||||||||
Db 51 RILAVERYLKDQQLGIGCGSKLIC 76

RESULT 288
Q90E69 PRELIMINARY; PRT; 163 AA.
AC Q90E69;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SC22;
RA Feng H., Huang Y., Yang D., Tang H., Hu X.;
RT "Phylogenetic analysis of part of env gene of HIV-1 isolates from Sichuan."
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY037961; AAK72334.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 163
SQ SEQUENCE 163 AA; 19200 MW; EF4E811ED3871087 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 163;
Best Local Similarity 96.2%; Pred. No. 2.6e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIGCGSKLIC 26
|:|||||||||||||||||

Db 51 RILAVERYLKDQQLGIGCGSKLIC 76

RESULT 289
Q90E73 PRELIMINARY; PRT; 163 AA.
ID Q90E73;
AC Q90E73;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SC03;
RA Feng H., Huang Y., Yang D., Tang H., Hu X.;
RT "Phylogenetic analysis of part of env gene of HIV-1 isolates from Sichuan."
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY037957; AAK72330.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 163
SQ SEQUENCE 163 AA; 19274 MW; 121PACDABCD75A0D CRC64;

Query Match 99.3%; Score 138; DB 15; Length 163;
Best Local Similarity 96.2%; Pred. No. 2.6e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIGCGSKLIC 26
|:|||||||||||||||||
Db 51 RILAVERYLKDQQLGIGCGSKLIC 76

RESULT 290
Q90E67 PRELIMINARY; PRT; 163 AA.
ID Q90E67;
AC Q90E67;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SC23;
RA Feng H., Huang Y., Yang D., Tang H., Hu X.;
RT "Phylogenetic analysis of part of env gene of HIV-1 isolates from Sichuan."
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY037963; AAK72336.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 163
SQ SEQUENCE 163 AA; 19200 MW; EF4E811ED3871087 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 163;

```
Best Local Similarity 96.2%; Pred. No. 2.6e-13; -
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RILAVERYLKDQQLGIWCGSGKLIC 26
Db 51 RVLAVERYLKDQQLGIWCGSGKLIC 76
:|||||
:|||||

RESULT 291
Q90E68 ID Q90E68 PRELIMINARY; PRT; 163 AA.
AC Q90E68;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SC26;
RA Feng H., Huang Y., Yang D., Tang H., Hu X.;
RT "Phylogenetic analysis of part of env gene of HIV-1 isolates from
RL Sichuan.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY037962; AAK72335.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Transmembrane.
FT NON_TER 1
FT NON_TER 163
FT SEQUENCE 163 AA; 19200 MW; EF4E811ED3871087 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 163;
Best Local Similarity 96.2%; Pred. No. 2.6e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RILAVERYLKDQQLGIWCGSGKLIC 26
Db 51 RVLAVERYLKDQQLGIWCGSGKLIC 76
:|||||
:|||||

RESULT 292
Q90E71 ID Q90E71 PRELIMINARY; PRT; 163 AA.
AC Q90E71;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SC19;
RA Feng H., Huang Y., Yang D., Tang H., Hu X.;
RT "Phylogenetic analysis of part of env gene of HIV-1 isolates from
RL Sichuan.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY037959; AAK72332.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Transmembrane.
FT NON_TER 1
FT NON_TER 163
FT SEQUENCE 163 AA; 19347 MW; C397B8BE5624A725 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 163;
Best Local Similarity 96.2%; Pred. No. 2.6e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RILAVERYLKDQQLGIWCGSGKLIC 26
Db 51 RVLAVERYLKDQQLGIWCGSGKLIC 76
:|||||
:|||||

RESULT 293
Q90E74 ID Q90E74 PRELIMINARY; PRT; 163 AA.
AC Q90E74;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SC18;
RA Feng H., Huang Y., Yang D., Tang H., Hu X.;
RT "Phylogenetic analysis of part of env gene of HIV-1 isolates from
RL Sichuan.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY037956; AAK72329.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Transmembrane.
FT NON_TER 1
FT NON_TER 163
FT SEQUENCE 163 AA; 19347 MW; C397B8BE5624A725 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 163;
Best Local Similarity 96.2%; Pred. No. 2.6e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RILAVERYLKDQQLGIWCGSGKLIC 26
Db 51 RVLAVERYLKDQQLGIWCGSGKLIC 76
:|||||
:|||||

RESULT 294
Q90E72 ID Q90E72 PRELIMINARY; PRT; 163 AA.
AC Q90E72;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SC24;
RA Feng H., Huang Y., Yang D., Tang H., Hu X.;
RT "Phylogenetic analysis of part of env gene of HIV-1 isolates from
RL Sichuan.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY037958; AAK72331.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
```

```
DR GO: GO:0019031; C:viral envelope; IEA.
DR GO: GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 163
SQ SEQUENCE 163 AA; 19370 MW; 82180C09173ADCA8 CRC64;

Query Match          99.3%; Score 138; DB 15; Length 163;
Best Local Similarity 96.2%; Pred. No. 2.6e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSGKLC 26
Db 51 RVLAVERYLKDQQLGIWCGSGKLC 76

RESULT 295
Q90E65 PRELIMINARY; PRT; 163 AA.
AC Q90E65;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SC05;
RA Feng H., Huang Y., Yang D., Tang H., Hu X.;
RT "Phylogenetic analysis of part of env gene of HIV-1 isolates from
RT Sichuan."
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY037965; AAK72338.1; -.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0019031; C:viral envelope; IEA.
DR GO: GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 163
SQ SEQUENCE 163 AA; 19324 MW; ED9E3D98EC3DFE74 CRC64;

Query Match          99.3%; Score 138; DB 15; Length 163;
Best Local Similarity 96.2%; Pred. No. 2.6e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSGKLC 26
Db 51 RVLAVERYLKDQQLGIWCGSGKLC 76

RESULT 296
Q8J3R2 PRELIMINARY; PRT; 164 AA.
AC Q8J3R2;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE GP41 protein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22092513; PubMed=12097573;
RA Boutonnet N., Janesens W., Boutton C., Verschelde J.L., Heyndrickx L.,

RA Beirnaert E., van der Groen G., Lesters I.;
RT "Comparison of predicted scaffold-compatible sequence variation in the
RT triple-hairpin structure of human immunodeficiency virus type 1 gp41
RT with patient data."
RL J. Virol. 76:7595-7606 (2002).
DR EMBL; AJ427991; CAD20943.1; -.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0019031; C:viral envelope; IEA.
DR GO: GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 164
SQ SEQUENCE 164 AA; 19291 MW; F91298D132E359C7 CRC64;

Query Match          99.3%; Score 138; DB 15; Length 164;
Best Local Similarity 96.2%; Pred. No. 2.6e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSGKLC 26
Db 44 RVLAVERYLKDQQLGIWCGSGKLC 69

RESULT 297
Q90E78 PRELIMINARY; PRT; 164 AA.
AC Q90E78;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SC13;
RA Feng H., Huang Y., Yang D., Tang H., Hu X.;
RT "Phylogenetic analysis of part of env gene of HIV-1 isolates from
RT Sichuan."
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY037952; AAK72325.1; -.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0019031; C:viral envelope; IEA.
DR GO: GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 164
SQ SEQUENCE 164 AA; 19224 MW; 078AD292ED08AC4F CRC64;

Query Match          99.3%; Score 138; DB 15; Length 164;
Best Local Similarity 96.2%; Pred. No. 2.6e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSGKLC 26
Db 52 RVLAVERYLKDQQLGIWCGSGKLC 77

RESULT 298
Q90E81 PRELIMINARY; PRT; 164 AA.
AC Q90E81;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
```

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OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SC29;
RA Feng H., Huang Y., Yang D., Tang H., Hu X.;
RT "Phylogenetic analysis of part of env gene of HIV-1 isolates from
RT Sichuan.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY037949; AAK72322.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Transmembrane.
KW NON_TER 1
FT NON_TER 164
SQ SEQUENCE 164 AA; 19272 MW; CC3567E17D3D322E CRC64;

Query Match 99.3%; Score 138; DB 15; Length 164;
Best Local Similarity 96.2%; Pred. No. 2.6e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RILAVERYLKDQQLGIWCGSGKLC 26
Db 52 RVLAVERYLKDQQLGIWCGSGKLC 77

RESULT 299
Q90E64
ID Q90E64 PRELIMINARY; PRT; 164 AA.
AC Q90E64;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SC16;
RA Feng H., Huang Y., Yang D., Tang H., Hu X.;
RT "Phylogenetic analysis of part of env gene of HIV-1 isolates from
RT Sichuan.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY037966; AAK72339.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Transmembrane.
KW NON_TER 1
FT NON_TER 164
SQ SEQUENCE 164 AA; 19389 MW; 505315DE3C2E2D87 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 164;
Best Local Similarity 96.2%; Pred. No. 2.6e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RILAVERYLKDQQLGIWCGSGKLC 26
Db 52 RVLAVERYLKDQQLGIWCGSGKLC 77

RESULT 300
Q90E70
ID Q90E70 PRELIMINARY; PRT; 164 AA.
AC Q90E70;
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DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SC20;
RA Feng H., Huang Y., Yang D., Tang H., Hu X.;
RT "Phylogenetic analysis of part of env gene of HIV-1 isolates from
RT Sichuan.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY037960; AAK72333.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Transmembrane.
KW NON_TER 1
FT NON_TER 164
SQ SEQUENCE 164 AA; 19249 MW; 4218E2E1AF2150EF CRC64;

Query Match 99.3%; Score 138; DB 15; Length 164;
Best Local Similarity 96.2%; Pred. No. 2.6e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RILAVERYLKDQQLGIWCGSGKLC 26
Db 52 RVLAVERYLKDQQLGIWCGSGKLC 77

RESULT 301
Q90E82
ID Q90E82 PRELIMINARY; PRT; 164 AA.
AC Q90E82;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SC02;
RA Feng H., Huang Y., Yang D., Tang H., Hu X.;
RT "Phylogenetic analysis of part of env gene of HIV-1 isolates from
RT Sichuan.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY037948; AAK72321.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Transmembrane.
KW NON_TER 1
FT NON_TER 164
SQ SEQUENCE 164 AA; 19246 MW; 0FC57937F2165F31 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 164;
Best Local Similarity 96.2%; Pred. No. 2.6e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RILAVERYLKDQQLGIWCGSGKLC 26
Db 52 RVLAVERYLKDQQLGIWCGSGKLC 77
```

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RESULT 302
Q8JER3
ID Q8JER3 PRELIMINARY; PRT; 180 AA.
AC Q8JER3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CDNR-1;
RA Poveda E., Rodes B., Toro C., Martin-Carbonero L., Soriano V.;
RT "Evolution of the env gene (gp41) in HIV-1 positive patients receiving
RT T-20, a fusion inhibitor.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF500087; AAM21673.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 180
SQ SEQUENCE 180 AA; 21017 MW; 5C1AE2C3D95AA49 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 180;
Best Local Similarity 96.2%; Pred. No. 2.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGWCSCGKLC 26
Db 51 RILAVERYLKDQQLGWCSCGKLC 76

RESULT 303
Q8JER4
ID Q8JER4 PRELIMINARY; PRT; 181 AA.
AC Q8JER4;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CDNR-0;
RA Poveda E., Rodes B., Toro C., Martin-Carbonero L., Soriano V.;
RT "Evolution of the env gene (gp41) in HIV-1 positive patients receiving
RT T-20, a fusion inhibitor.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF500086; AAM21672.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 181
SQ SEQUENCE 181 AA; 21126 MW; 27DF2E95E885C2AA CRC64;

Query Match 99.3%; Score 138; DB 15; Length 181;
Best Local Similarity 96.2%; Pred. No. 2.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGWCSCGKLC 26
Db 51 RILAVERYLKDQQLGWCSCGKLC 76

RESULT 304
Q8JAK8
ID Q8JAK8 PRELIMINARY; PRT; 188 AA.
AC Q8JAK8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=96BRRJ101;
RA Guimaraes M.L., Moreira A.S., Loureiro R., Galvao-Castro B.,
RA Morgado M.G.;
RT "High frequency of recombinant genomes in HIV-1 samples from Brazilian
RT Southeastern and Southern regions.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF463436; AAM90812.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 188
SQ SEQUENCE 188 AA; 21441 MW; 80D9C61680E67E35 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 188;
Best Local Similarity 96.2%; Pred. No. 3e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGWCSCGKLC 26
Db 87 RILAVERYLKDQQLGWCSCGKLC 112

RESULT 305
Q8JAJ7
ID Q8JAJ7 PRELIMINARY; PRT; 190 AA.
AC Q8JAJ7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=95BRSP001;
RA Guimaraes M.L., Moreira A.S., Loureiro R., Galvao-Castro B.,
RA Morgado M.G.;
RT "High frequency of recombinant genomes in HIV-1 samples from Brazilian
RT Southeastern and Southern regions.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF463447; AAM90823.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
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Db 51 RILAVERYLKDQQLGWCSCGKLC 76
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DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR KEGG; K01190; GP120; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 190 190
FT NON_TER 190 190
SQ SEQUENCE 190 AA; 21717 MW; BDA818CAB5A9329F CRC64;

Query Match 99.3%; Score 138; DB 15; Length 190;
Best Local Similarity 96.2%; Pred. No. 3.1e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RILAVERYLKDQQLGIWCGSKLIC 26
Db 93 RVLAVERYLKDQQLGIWCGSKLIC 118

RESULT 306
Q8JAL2 PRELIMINARY; PRT; 192 AA.
AC Q8JAL2;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=95BRJ019;
RA Guimaraes M.L., Moreira A.S., Loureiro R., Galvao-Castro B.,
Morgado M.G.;
RT "High frequency of recombinant genomes in HIV-1 samples from Brazilian
Southeastern and Southern regions.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF463432; AM90808.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 192 192
FT NON_TER 192 192
SQ SEQUENCE 192 AA; 22182 MW; 357E8C354BD97D1A CRC64;

Query Match 99.3%; Score 138; DB 15; Length 192;
Best Local Similarity 96.2%; Pred. No. 3.1e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RILAVERYLKDQQLGIWCGSKLIC 26
Db 83 RVLAVERYLKDQQLGIWCGSKLIC 108

RESULT 307
Q8JAL3 PRELIMINARY; PRT; 199 AA.
AC Q8JAL3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=95BRJ019;
RA Guimaraes M.L., Moreira A.S., Loureiro R., Galvao-Castro B.,
Morgado M.G.;
RT "High frequency of recombinant genomes in HIV-1 samples from Brazilian
Southeastern and Southern regions.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF463432; AM90808.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 199 199
FT NON_TER 199 199
SQ SEQUENCE 199 AA; 22918 MW; F6AA8478D3305BC7 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 199;
Best Local Similarity 96.2%; Pred. No. 3.2e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RILAVERYLKDQQLGIWCGSKLIC 26
Db 102 RVLAVERYLKDQQLGIWCGSKLIC 127

RESULT 308
Q8JAL5 PRELIMINARY; PRT; 201 AA.
AC Q8JAL5;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=95BRJ017;
RA Guimaraes M.L., Moreira A.S., Loureiro R., Galvao-Castro B.,
Morgado M.G.;
RT "High frequency of recombinant genomes in HIV-1 samples from Brazilian
Southeastern and Southern regions.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF463429; AM90805.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 201 201
FT NON_TER 201 201
SQ SEQUENCE 201 AA; 23181 MW; B3AD0929DEC8020D CRC64;

Query Match 99.3%; Score 138; DB 15; Length 201;
Best Local Similarity 96.2%; Pred. No. 3.3e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RILAVERYLKDQQLGIWCGSKLIC 26
Db 92 RVLAVERYLKDQQLGIWCGSKLIC 117
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RESULT 309
Q8JAL8
ID Q8JAL8 PRELIMINARY; PRT; 201 AA.
AC Q8JAL8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=95BRJ013;
RA Guimaraes M.L., Moreira A.S., Loureiro R., Galvao-Castro B.,
RA Morgado M.G.;
RT "High frequency of recombinant genomes in HIV-1 samples from Brazilian
RT Southeastern and Southern regions.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF463426; AM90802.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 201
SQ SEQUENCE 201 AA; 23281 MW; 67ABC2E7D2C93B44 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 201;
Best Local Similarity 96.2%; Pred. No. 3.3e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCSGKLC 26
|:|||||
Db 98 RVLAVERYLKDQQLGIWCSGKLC 123

RESULT 310
Q8JAM0
ID Q8JAM0 PRELIMINARY; PRT; 217 AA.
AC Q8JAM0;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=95BRJ011;
RA Guimaraes M.L., Moreira A.S., Loureiro R., Galvao-Castro B.,
RA Morgado M.G.;
RT "High frequency of recombinant genomes in HIV-1 samples from Brazilian
RT Southeastern and Southern regions.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF463424; AM90800.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
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KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 217
SQ SEQUENCE 217 AA; 24952 MW; 3F41BA3210A46167 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 217;
Best Local Similarity 96.2%; Pred. No. 3.5e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCSGKLC 26
|:|||||
Db 117 RVLAVERYLKDQQLGIWCSGKLC 142

RESULT 311
Q99IC1
ID Q99IC1 PRELIMINARY; PRT; 225 AA.
AC Q99IC1;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope polyprotein (Fragment).
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Ishiko H., West K., Zeng W., Spaulding A., Islam S., Norman J.,
RA Zivny I., Jaray W., Pozzi L., Kurane I., Ennis F.;
RT "Autologous HIV-1-specific cytotoxic T lymphocytes (CTL) established
RT at two different time points: Role of CTL in the emergence of escaped
RT mutants.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB047355; BAB32636.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR Pfam; PF00517; GP41; 1.
KW Polyprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 225
SQ SEQUENCE 225 AA; 25618 MW; B8A1E50F503D2A9A CRC64;

Query Match 99.3%; Score 138; DB 15; Length 225;
Best Local Similarity 96.2%; Pred. No. 3.7e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCSGKLC 26
|:|||||
Db 68 RVLAVERYLKDQQLGIWCSGKLC 93

RESULT 312
Q99IB9
ID Q99IB9 PRELIMINARY; PRT; 225 AA.
AC Q99IB9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope polyprotein (Fragment).
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Ishiko H., West K., Zeng W., Spaulding A., Islam S., Norman J.,
RA Zivny I., Jaray W., Pozzi L., Kurane I., Ennis F.;
RT "Autologous HIV-1-specific cytotoxic T lymphocytes (CTL) established
RT at two different time points: Role of CTL in the emergence of escaped
RT mutants.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB047357; BAB32638.1; -.

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DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Polypeptide; Transmembrane.
FT NON_TER 225 225
FT NON_TER 225 225
SQ SEQUENCE 225 AA; 25557 MW; C5660AB589DDFA6 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 225;
Best Local Similarity 96.2%; Pred. No. 3.7e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSKGLIC 26
Db 68 RVLAVERYLKDQQLGIWCGSKGLIC 93

RESULT 313
Q99IC4 ID Q99IC4 PRELIMINARY; PRT; 225 AA.
AC Q99IC4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope polypeptide (Fragment).
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Ishiko H., West K., Zeng W., Spaulding A., Islam S., Norman J.,
RA Zivny I., Jaray W., Pozzi L., Kurane I., Ennis F.;
RT "Autologous HIV-1-specific cytotoxic T lymphocytes (CTL) established
RT at two different time points: Role of CTL in the emergence of escaped
RT mutants.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB047352; BAB32633.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Polypeptide; Transmembrane.
FT NON_TER 225 225
FT NON_TER 225 225
SQ SEQUENCE 225 AA; 25480 MW; C2166441900478ED CRC64;

Query Match 99.3%; Score 138; DB 15; Length 225;
Best Local Similarity 96.2%; Pred. No. 3.7e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSKGLIC 26
Db 68 RVLAVERYLKDQQLGIWCGSKGLIC 93

RESULT 314
Q99IC3 ID Q99IC3 PRELIMINARY; PRT; 225 AA.
AC Q99IC3;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope polypeptide (Fragment).
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Ishiko H., West K., Zeng W., Spaulding A., Islam S., Norman J.,
RA Zivny I., Jaray W., Pozzi L., Kurane I., Ennis F.;
RT "Autologous HIV-1-specific cytotoxic T lymphocytes (CTL) established
RT at two different time points: Role of CTL in the emergence of escaped
RT mutants.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB047352; BAB32633.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Polypeptide; Transmembrane.
FT NON_TER 225 225
FT NON_TER 225 225
SQ SEQUENCE 225 AA; 25480 MW; C2166441900478ED CRC64;

Query Match 99.3%; Score 138; DB 15; Length 225;
Best Local Similarity 96.2%; Pred. No. 3.7e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSKGLIC 26
Db 68 RVLAVERYLKDQQLGIWCGSKGLIC 93

RESULT 315
Q99IC5 ID Q99IC5 PRELIMINARY; PRT; 225 AA.
AC Q99IC5;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope polypeptide (Fragment).
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Ishiko H., West K., Zeng W., Spaulding A., Islam S., Norman J.,
RA Zivny I., Jaray W., Pozzi L., Kurane I., Ennis F.;
RT "Autologous HIV-1-specific cytotoxic T lymphocytes (CTL) established
RT at two different time points: Role of CTL in the emergence of escaped
RT mutants.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB047351; BAB32632.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Polypeptide; Transmembrane.
FT NON_TER 225 225
FT NON_TER 225 225
SQ SEQUENCE 225 AA; 25527 MW; EB6B83E37AD63B04 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 225;
Best Local Similarity 96.2%; Pred. No. 3.7e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSKGLIC 26
Db 68 RVLAVERYLKDQQLGIWCGSKGLIC 93

RESULT 316
Q99IC0 ID Q99IC0 PRELIMINARY; PRT; 225 AA.
AC Q99IC0;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope polypeptide (Fragment).
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.

RT "Autologous HIV-1-specific cytotoxic T lymphocytes (CTL) established
RT at two different time points: Role of CTL in the emergence of escaped
RT mutants.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB047353; BAB32634.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Polypeptide; Transmembrane.
FT NON_TER 225 225
FT NON_TER 225 225
SQ SEQUENCE 225 AA; 25609 MW; 6C1A3A0334931031 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 225;
Best Local Similarity 96.2%; Pred. No. 3.7e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSKGLIC 26
Db 68 RVLAVERYLKDQQLGIWCGSKGLIC 93

RESULT 315
Q99IC5 ID Q99IC5 PRELIMINARY; PRT; 225 AA.
AC Q99IC5;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope polypeptide (Fragment).
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Ishiko H., West K., Zeng W., Spaulding A., Islam S., Norman J.,
RA Zivny I., Jaray W., Pozzi L., Kurane I., Ennis F.;
RT "Autologous HIV-1-specific cytotoxic T lymphocytes (CTL) established
RT at two different time points: Role of CTL in the emergence of escaped
RT mutants.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB047351; BAB32632.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Polypeptide; Transmembrane.
FT NON_TER 225 225
FT NON_TER 225 225
SQ SEQUENCE 225 AA; 25527 MW; EB6B83E37AD63B04 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 225;
Best Local Similarity 96.2%; Pred. No. 3.7e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSKGLIC 26
Db 68 RVLAVERYLKDQQLGIWCGSKGLIC 93

RESULT 316
Q99IC0 ID Q99IC0 PRELIMINARY; PRT; 225 AA.
AC Q99IC0;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope polypeptide (Fragment).
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.


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OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Ishiko H., West K., Zeng W., Spaulding A., Islam S., Norman J.,
RA Zivny I., Jarry W., Pozzi L., Kurane I., Ennis F.;
RA "Autologous HIV-1-specific cytotoxic T lymphocytes (CTL) established
RT at two different time points: Role of CTL in the emergence of escaped
RT mutants.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBDJ databases.
DR EMBL; AB047356; BAB32637.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Polyprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 225
SQ SEQUENCE 225 AA; 25579 MW; B9013F57411CDBC CRC64;

Query Match 99.3%; Score 138; DB 15; Length 225;
Best Local Similarity 96.2%; Pred. No. 3.7e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIGCSGKLC 26
DB 68 RVLAVERYLKDQQLGIGCSGKLC 93

RESULT 317
Q78118 ID Q78118 PRELIMINARY; PRT; 357 AA.
AC Q78118;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope protein, gp120 /gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=92144209; PubMed=1736940;
RA Steuler H., Storch-Hagenlocher B., Wildemann B.;
RA "Distinct populations of Human immunodeficiency virus type 1 in blood
RT and cerebrospinal fluid.";
RL AIDS Res. Hum. Retroviruses 8:53-59 (1992).
DR EMBL; X61355; CAA43622.1; -.
DR PIR; S21994; S21994.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 225
SQ SEQUENCE 357 AA; 41140 MW; CE87EB06A73CDCA4 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 357;
Best Local Similarity 96.2%; Pred. No. 5.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIGCSGKLC 26
DB 80 RVLAVERYLKDQQLGIGCSGKLC 105

RESULT 318
Q78156 ID Q78156 PRELIMINARY; PRT; 357 AA.
AC Q78156;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope protein, gp120 /gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=92144209; PubMed=1736940;
RA Steuler H., Storch-Hagenlocher B., Wildemann B.;
RA "Distinct populations of Human immunodeficiency virus type 1 in blood
RT and cerebrospinal fluid.";
RL AIDS Res. Hum. Retroviruses 8:53-59 (1992).
DR EMBL; X61355; CAA43622.1; -.
DR PIR; S21994; S21994.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 225
SQ SEQUENCE 357 AA; 41140 MW; CE87EB06A73CDCA4 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 357;
Best Local Similarity 96.2%; Pred. No. 5.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIGCSGKLC 26
DB 80 RVLAVERYLKDQQLGIGCSGKLC 105

RESULT 319
Q78112 ID Q78112 PRELIMINARY; PRT; 357 AA.
AC Q78112;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope protein, gp120 /gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=92144209; PubMed=1736940;
RA Steuler H., Storch-Hagenlocher B., Wildemann B.;
RA "Distinct populations of Human immunodeficiency virus type 1 in blood
RT and cerebrospinal fluid.";
RL AIDS Res. Hum. Retroviruses 8:53-59 (1992).
DR EMBL; X61358; CAA43628.1; -.
DR PIR; S70424; S21992.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 357
SQ SEQUENCE 357 AA; 41248 MW; C3E22F3EF8C4847E CRC64;

Query Match 99.3%; Score 138; DB 15; Length 357;
Best Local Similarity 96.2%; Pred. No. 5.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIGCSGKLC 26
DB 80 RVLAVERYLKDQQLGIGCSGKLC 105
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RESULT 320
Q78155 ID Q78155 PRELIMINARY; PRT; 357 AA.
AC Q78155;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope protein, gp120 /gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92144209; PubMed=1736940;
RA Steuler H., Storch-Hagenlocher B., Wildemann B.;
RT "Distinct populations of Human immunodeficiency virus type 1 in blood
RT and cerebrospinal fluid."
RL AIDS Res. Hum. Retroviruses 8:53-59(1992).
DR EMBL; X61353; CAA43618.1; -.
DR PIR; A53591; A53591.
DR PIR; S22004; S22004.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
SQ SEQUENCE 357 AA; 41152 MW; 07462A9B4505C734 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 357;
Best Local Similarity 96.2%; Pred. No. 5.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSKGLIC 26
Db 80 RVLAVERYLKDQQLGIWCGSKGLIC 105

RESULT 321
Q9WIT0 ID Q9WIT0 PRELIMINARY; PRT; 362 AA.
AC Q9WIT0;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp41 protein (fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20092438; PubMed=10628816;
RA Jonassen T.O., Grinde B., Asjo B., Hasle G., Hungenes O.;
RT "Inter-subtype recombinant HIV-1 involving HIV-MAL-like and subtype H-
RT like sequence in four Norwegian cases."
RL AIDS Res. Hum. Retroviruses 16:49-58(2000).
DR EMBL; AJ237569; CAB39745.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 1
SQ SEQUENCE 362 AA; 41388 MW; E5DFF443EC39FFED CRC64;
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Query Match 99.3%; Score 138; DB 15; Length 362;
Best Local Similarity 96.2%; Pred. No. 6e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSKGLIC 26
Db 86 RVLAVERYLKDQQLGIWCGSKGLIC 111

RESULT 322
Q8QDX2 ID Q8QDX2 PRELIMINARY; PRT; 380 AA.
AC Q8QDX2;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=98BY10443;
RA Masharsky A.E., Eremin V.F., Kozlov A.P.;
RT "Molecular cloning and analysis of full-length human immunodeficiency
RT virus type 1 genomes of prevalent strains among IDUs in countries of
RT the FSU."
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF414005; AAL78485.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 1
SQ SEQUENCE 380 AA; 43859 MW; 42B1798C20603F06 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 380;
Best Local Similarity 96.2%; Pred. No. 6.3e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSKGLIC 26
Db 103 RVLAVERYLKDQQLGIWCGSKGLIC 128

RESULT 323
Q8QE11 ID Q8QE11 PRELIMINARY; PRT; 387 AA.
AC Q8QE11;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=98UA0116;
RA Masharsky A.E., Eremin V.F., Kozlov A.P.;
RT "Molecular cloning and analysis of full-length human immunodeficiency
RT virus type 1 genomes of prevalent strains among IDUs in countries of
RT the FSU."
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF413981; AAL78436.1; -.
```

DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 1
SQ SEQUENCE 387 AA; 43919 MW; 84FEB68CB64FA44 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 387;
Best Local Similarity 96.2%; Pred. No. 6.4e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGWCSGKLC 26
|:|||||
DB 103 RVLAVERYLKDQQLGWCSGKLC 128

RESULT 324

Q8QE15 PRELIMINARY; PRT; 387 AA.
AC Q8QE15;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=98UA0116;
RA Masharsky A.E., Eremin V.F., Kozlov A.P.;
RT "Molecular cloning and analysis of full-length human immunodeficiency virus type 1 genomes of prevalent strains among IDUs in countries of the FSU";
RT the FSU.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF413980; AAL78430.1; -;
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 1
SQ SEQUENCE 387 AA; 44021 MW; 93B05A2C598B01C1 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 387;
Best Local Similarity 96.2%; Pred. No. 6.4e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGWCSGKLC 26
|:|||||
DB 103 RVLAVERYLKDQQLGWCSGKLC 128

RESULT 325

Q8QE07 PRELIMINARY; PRT; 387 AA.
AC Q8QE07;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.

OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=98UA0116;
RA Masharsky A.E., Eremin V.F., Kozlov A.P.;
RT "Molecular cloning and analysis of full-length human immunodeficiency virus type 1 genomes of prevalent strains among IDUs in countries of the FSU";
RT the FSU.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF413982; AAL78438.1; -;
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 1
SQ SEQUENCE 387 AA; 44020 MW; 4E58E7273CA1E050 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 387;
Best Local Similarity 96.2%; Pred. No. 6.4e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGWCSGKLC 26
|:|||||
DB 103 RVLAVERYLKDQQLGWCSGKLC 128

RESULT 326

Q8J511 PRELIMINARY; PRT; 392 AA.
AC Q8J511;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=95BRJ014;
RA Guimaraes M.L., Moreira A.S., Loureiro R., Galvao-Castro B., Morgado M.G.;
RT "High Frequency of Recombinant Genomes in HIV-1 Samples From Brazilian Southeastern and Southern Regions";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; AY072000; AAL62003.1; -;
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 1
SQ SEQUENCE 392 AA; 44221 MW; 67B9E800167DAE02 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 392;
Best Local Similarity 96.2%; Pred. No. 6.5e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGWCSGKLC 26
|:|||||
DB 302 RVLAVERYLKDQQLGWCSGKLC 327

Bongertz V., Bou-Habib D.C., Brígido L.F.M., Caseiro M., Chequer P.J., Couto-Fernandez J.C., Ferreira P.C., Galvao-Castro B., Greco D., Guimarães M.L., Linhares de Carvalho M.I., Morgado M.G., Oliveira C.A., Osmanov S., Ramos C.A., Rossini M., Sabino E., Tanuri A., Ueda M.;
"HIV-1 diversity in Brazil: genetic, biologic, and immunologic characterization of HIV-1 strains in three potential HIV vaccine evaluation sites. Brazilian Network for HIV Isolation and Characterization.";
J. Acquir. Immune Defic. Syndr. 23:184-193(2000).
[2]
SEQUENCE FROM N.A.
STRAIN=95BRSP004;
Guimaraes M.;
"High frequency of HIV-1 recombinant genomes in samples from southeast RT and south regions of Brazil.";
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF062423; AAC17162.2; -.
PIR; A53591; A53591.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; ENV GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane. 1
FT NON_TER 1
FT FT 416 416
SQ SEQUENCE 416 AA; 47011 MW; 3E6244DFAC4A8703 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 416;
Best Local Similarity 96.2%; Pred.No. 6.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps

Qy 1 RLAVERYLKDQLLGWCGSKLIC 26
|:|||||||
Db 305 RVLAVERYLKDQLLGWCGSKLIC 330

RESULT 329
ID ID Q8J513 PRELIMINARY; PRT; 416 AA.
AC Q8J513;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OC Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxId=11676;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=95BRSP004;
RA Guimaraes M.L.; Moreira A.S., Loureiro R., Galvao-Castro B., Morgado M.G.;
RT "High Frequency of Recombinant Genomes in HIV-1 Samples From Brazilian RT Southeastern and Southern Regions.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR ENML; AY071998; AL62001.1; -.
DR PIR; A53591; A53591.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; ENV GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 1 416
FT FT 416 416

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SQ SEQUENCE 416 AA; 47011 MW; 3E244DFAC4A8703 CRC64;
Query Match 99.3%; Score 138; DB 15; Length 416;
Best Local Similarity 96.2%; Pred. No. 6.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGICGSGKLC 26
DB 305 RVLAVERYLKDQQLGICGSGKLC 330

RESULT 330
Q83514
ID Q8J514 PRELIMINARY; PRT; 421 AA.
AC Q8J514;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=96BRRJ01;
RA Guimaraes M.L., Moreira A.S., Loureiro R., Galvao-Castro B.,
RA Morgado M.G.;
RT "High Frequency of Recombinant Genomes in HIV-1 Samples From Brazilian
RT Southeastern and Southern Regions";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY071997; AAL62000.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 421
SQ SEQUENCE 421 AA; 47597 MW; FE05A7E3071758CB CRC64;

Query Match 99.3%; Score 138; DB 15; Length 421;
Best Local Similarity 96.2%; Pred. No. 7e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGICGSGKLC 26
DB 310 RVLAVERYLKDQQLGICGSGKLC 335

RESULT 331
O41643
ID O41643 PRELIMINARY; PRT; 546 AA.
AC O41643;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PC12;
RX MEDLINE=98105804; PubMed=9445059;
RA Connor R.I., Korber B.T.M., Graham B.S., Hahn B.H., Ho D.D.,
RA Walker B.D., Neumann A.U., Vermund S.H., Mestecky J., Jackson S.,
RA Fenamore E., Cao Y., Gao F., Kalam S., Kunstman K.J., McDonald D.,
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McWilliams N., Trkola A., Moore J.P., Wolinsky S.M.;
RT "Immunological and virological analyses of persons infected by human
RT recombinant gp120 subunit vaccines.";
RL J. Virol. 72:1552-1576(1998).
DR EMBL; U84885; AAC58931.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 546
SQ SEQUENCE 546 AA; 61591 MW; B7273DB04581D451 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 546;
Best Local Similarity 96.2%; Pred. No. 9.2e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGICGSGKLC 26
DB 448 RVLAVERYLKDQQLGICGSGKLC 473

RESULT 332
Q73363
ID Q73363 PRELIMINARY; PRT; 605 AA.
AC Q73363;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein.
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TH/93/67;
RX MEDLINE=96303593; PubMed=8744585;
RA Penny M.A., Thomas S.J., Douglas N.W., Ranjbar S., Holmes H.,
RA Daniels R.S.;
RT "env gene sequences of primary HIV type 1 isolates of subtypes B, C,
RT D, E, and F obtained from the World Health Organization Network for
RT HIV Isolation and Characterization.";
RL AIDS Res. Hum. Retroviruses 12:741-747(1996).
DR EMBL; U39258; AAB37195.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
SQ SEQUENCE 605 AA; 67420 MW; B384ACADA15AB6FB CRC64;

Query Match 99.3%; Score 138; DB 15; Length 605;
Best Local Similarity 96.2%; Pred. No. 1e-12;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGICGSGKLC 26
DB 562 RVLAVERYLKDQQLGICGSGKLC 587

RESULT 333
Q9Q6V8
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ID Q9C6V8 PRELIMINARY; PRT; 606 AA.
AC Q9C6V8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Truncated envelope glycoprotein.
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KAL153;
RX MEDLINE=20386750; PubMed=10933619;
RA Liitsola K., Holm K., Bobkov A., Pokrovski V., Smolskaja T.,
RA Leinikki P., Osmanov S., Salminen M., UNAIDS Virus Isolation Network;
RT "An AB recombinant and its parental HIV type 1 strains in the area of
RT the former soviet union: low requirements for sequence identity in
RT recombination.";
RL AIDS Res. Hum. Retroviruses 16:1047-1053(2000).
[2]
RN SEQUENCE FROM N.A.
RP STRAIN=KAL153;
RA Liitsola K.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF193276; AAF22321.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Polyprotein;
KW Transmembrane.
KW SEQUENCE 606 AA; 67781 MW; 218C77457D4DFA8A CRC64;

Query Match 99.3%; Score 138; DB 15; Length 606;
Best Local Similarity 96.2%; Pred. No. 1e-12; Indels 0; Gaps 0;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSKLIC 26
|:|||||
Db 563 RVLAVERYLKDQQLGIWCGSKLIC 588

RESULT 334
Q8Q859 PRELIMINARY; PRT; 616 AA.
AC Q8Q859;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE GP160.
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KR6035;
RA Daniels R.S., Patel D., Xiang Z., Zheng N.N., Kang C.;
RT "Evidence for the spread of immune-escape HIV-1 subtype B in the
RT Korean population.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; A3417419; CAD10131.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.

DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
SQ SEQUENCE 616 AA; 68756 MW; B855DAE5BA59BC15 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 616;
Best Local Similarity 96.2%; Pred. No. 1e-12; Indels 0; Gaps 0;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSKLIC 26
|:|||||
Db 586 RVLAVERYLKDQQLGIWCGSKLIC 611

RESULT 335
Q9IK02 PRELIMINARY; PRT; 679 AA.
AC Q9IK02;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Truncated envelope glycoprotein.
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=546hc-F7;
RA Gartner S., Liu Y., Tang X.P., McArthur J.C., Scott J.;
RT "Analysis of human immunodeficiency virus type 1 gp160 sequences from
RT a patient with HIV dementia: evidence for monocyte trafficking into
RT brain.";
RL J. Neurovirol. 0:0-0(2000).
DR EMBL; AF217165; AAF75507.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Polyprotein;
KW Transmembrane.
KW SEQUENCE 679 AA; 76494 MW; 69C6485D07902578 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 679;
Best Local Similarity 96.2%; Pred. No. 1.2e-12;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSKLIC 26
|:|||||
Db 584 RVLAVERYLKDQQLGIWCGSKLIC 609

RESULT 336
Q9IK06 PRELIMINARY; PRT; 684 AA.
AC Q9IK06;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein.
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=546hc-B6;
RA Gartner S., Liu Y., Tang X.P., McArthur J.C., Scott J.;
RT "Analysis of human immunodeficiency virus type 1 gp160 sequences from

```
RT a patient with HIV dementia: evidence for monocyte trafficking into
RL brain."
RL J. Neurovirol. 0:0-0(2000).
DR EMBL; AF217161; AAF75503.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env.GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
SQ SEQUENCE 684 AA; 77266 MW; F9EGF3CE4D32E10 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 684;
Best Local Similarity 96.2%; Pred. No. 1.2e-12;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGWSGKGLIC 26
Db 584 RVLAVERYLKDQQLGWSGKGLIC 609

RESULT 337
ID Q8Q856 PRELIMINARY; PRT; 729 AA.
AC Q8Q856;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp160.
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KRA812;
RA Daniels R.S., Patel D., Xiang Z., Zheng N.N., Kang C.;
RT "Evidence for the spread of immune-escape HIV-1 subtype B in the
RT Korean population."
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; AJ417422; CAD10134.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env.GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
SQ SEQUENCE 729 AA; 81920 MW; 97DA9CA263270381 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 729;
Best Local Similarity 96.2%; Pred. No. 1.2e-12;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGWSGKGLIC 26
Db 590 RVLAVERYLKDQQLGWSGKGLIC 615

RESULT 338
ID Q91W14 PRELIMINARY; PRT; 797 AA.
AC Q91W14;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp160.
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KRA812;
RA Daniels R.S., Patel D., Xiang Z., Zheng N.N., Kang C.;
RT "Evidence for the spread of immune-escape HIV-1 subtype B in the
RT Korean population."
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; AJ417422; CAD10134.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env.GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
SQ SEQUENCE 729 AA; 81920 MW; 97DA9CA263270381 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 729;
Best Local Similarity 96.2%; Pred. No. 1.2e-12;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGWSGKGLIC 26
Db 590 RVLAVERYLKDQQLGWSGKGLIC 615

RESULT 339
ID Q03808 PRELIMINARY; PRT; 797 AA.
AC Q03808;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein 120/41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=88302422; PubMed=2841608;
RA Fisher A.G., Ensoli B., Looney D., Rose A., Gallo R.C., Saag M.S.,
RA Shaw G.M., Hahn B.H., Wong-Staal F.;
RT "Biologically diverse molecular variants within a single HIV-1
RT isolate."
RL Nature 334:444-447(1988).
RN [2]
RP SEQUENCE FROM N.A.
RC MEDLINE=91374618; PubMed=1895406;
RA Daniels R.S., Smith M.H., Fisher A.G.;
RT "Molecular characterization of biologically diverse envelope variants
RT of human immunodeficiency virus type 1 derived from an individual."
RL J. Virol. 65:5574-5578(1991).
DR EMBL; M37575; AAB04111.1; -.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env.GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
FT NON TER 797
SQ SEQUENCE 797 AA; 90597 MW; F1BCF5B6FD6EB92A CRC64;

Query Match 99.3%; Score 138; DB 15; Length 797;
Best Local Similarity 96.2%; Pred. No. 1.4e-12;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=subtype B;
RA Daniels R.S., Beddows S., Wilson P., Douglas N.W., Patel D.,
RA Ives K.J., Easterbrook P., Weber J.N.;
RT "An association between amino acid substitutions in the 'Silent Face'
RT of Human immunodeficiency virus type 1 gp120 and resistance to
RT antibody mediated neutralization."
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ271111; CAB86164.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env.GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
SQ SEQUENCE 797 AA; 90755 MW; E08DDB15846ED4F7 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 797;
Best Local Similarity 96.2%; Pred. No. 1.4e-12;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGWSGKGLIC 26
Db 581 RVLAVERYLKDQQLGWSGKGLIC 606

RESULT 339
ID Q03808 PRELIMINARY; PRT; 797 AA.
AC Q03808;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein 120/41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=88302422; PubMed=2841608;
RA Fisher A.G., Ensoli B., Looney D., Rose A., Gallo R.C., Saag M.S.,
RA Shaw G.M., Hahn B.H., Wong-Staal F.;
RT "Biologically diverse molecular variants within a single HIV-1
RT isolate."
RL Nature 334:444-447(1988).
RN [2]
RP SEQUENCE FROM N.A.
RC MEDLINE=91374618; PubMed=1895406;
RA Daniels R.S., Smith M.H., Fisher A.G.;
RT "Molecular characterization of biologically diverse envelope variants
RT of human immunodeficiency virus type 1 derived from an individual."
RL J. Virol. 65:5574-5578(1991).
DR EMBL; M37575; AAB04111.1; -.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env.GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
FT NON TER 797
SQ SEQUENCE 797 AA; 90597 MW; F1BCF5B6FD6EB92A CRC64;

Query Match 99.3%; Score 138; DB 15; Length 797;
Best Local Similarity 96.2%; Pred. No. 1.4e-12;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY 1 RILAVERYLKDQQLGIWCGSKLIC 26
|:|||||
Db 572 RVLAVERYLKDQQLGIWCGSKLIC 597

RESULT 340

Q03810
ID Q03810 PRELIMINARY; PRT; 797 AA.
AC Q03810;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein 120/41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8302422; PubMed=2841608;
RA Fisher A.G., Ensoli B., Looney D., Rose A., Gallo R.C., Saag M.S.,
Shaw G.M., Hahn B.H., Wong-Staal F.;
RT "Biologically diverse molecular variants within a single HIV-1
isolate.";
RL Nature 334:444-447 (1988).
RN [2]

QY 1 RILAVERYLKDQQLGIWCGSKLIC 26
|:|||||
Db 572 RVLAVERYLKDQQLGIWCGSKLIC 597

Query Match 99.3%; Score 138; DB 15; Length 797;
Best Local Similarity 96.2%; Pred. No. 1.4e-12;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSKLIC 26
|:|||||
Db 572 RVLAVERYLKDQQLGIWCGSKLIC 597

RESULT 341

Q03807
ID Q03807 PRELIMINARY; PRT; 799 AA.
AC Q03807;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein 120/41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8302422; PubMed=2841608;
RA Fisher A.G., Ensoli B., Looney D., Rose A., Gallo R.C., Saag M.S.,
Shaw G.M., Hahn B.H., Wong-Staal F.;
RT "Biologically diverse molecular variants within a single HIV-1
isolate.";
RL Nature 334:444-447 (1988).
RN [2]

RP SEQUENCE FROM N.A.
RX MEDLINE=91374618; PubMed=1895406;
RA Daniels R.S., Smith M.H., Fisher A.G.;
RT "Molecular characterization of biologically diverse envelope variants
of human immunodeficiency virus type 1 derived from an individual.";
RL J. Virol. 65:5574-5578 (1991).
DR EMBL; M37574; AAB04110.1; -.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
FT NON_TER 799
SQ SEQUENCE 799 AA; 90630 MW; 9BE98E53F795327C CRC64;

Query Match 99.3%; Score 138; DB 15; Length 799;
Best Local Similarity 96.2%; Pred. No. 1.4e-12;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSKLIC 26
|:|||||
Db 574 RVLAVERYLKDQQLGIWCGSKLIC 599

RESULT 342

Q03809
ID Q03809 PRELIMINARY; PRT; 801 AA.
AC Q03809;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein 120/41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8302422;
RA Fisher A.G., Ensoli B., Looney D., Rose A., Gallo R.C., Saag M.S.,
Shaw G.M., Hahn B.H., Wong-Staal F.;
RT "Biologically diverse molecular variants within a single HIV-1
isolate.";
RL Nature 334:444-447 (1988).
RN [2]

QY 1 RILAVERYLKDQQLGIWCGSKLIC 26
|:|||||
Db 574 RVLAVERYLKDQQLGIWCGSKLIC 599

Query Match 99.3%; Score 138; DB 15; Length 797;
Best Local Similarity 96.2%; Pred. No. 1.4e-12;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSKLIC 26
|:|||||
Db 572 RVLAVERYLKDQQLGIWCGSKLIC 597

RESULT 341

Q03807
ID Q03807 PRELIMINARY; PRT; 799 AA.
AC Q03807;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein 120/41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8302422; PubMed=2841608;
RA Fisher A.G., Ensoli B., Looney D., Rose A., Gallo R.C., Saag M.S.,
Shaw G.M., Hahn B.H., Wong-Staal F.;
RT "Biologically diverse molecular variants within a single HIV-1
isolate.";
RL Nature 334:444-447 (1988).
RN [2]

RP SEQUENCE FROM N.A.
RX MEDLINE=91374618; PubMed=1895406;
RA Daniels R.S., Smith M.H., Fisher A.G.;
RT "Molecular characterization of biologically diverse envelope variants
of human immunodeficiency virus type 1 derived from an individual.";
RL J. Virol. 65:5574-5578 (1991).
DR EMBL; M37491; AAB04109.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
DR AIDS; Coats protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 801
SQ SEQUENCE 801 AA; 90891 MW; 5BF97B938EC4413 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 801;
Best Local Similarity 96.2%; Pred. No. 1.4e-12;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSKLIC 26
|:|||||
Db 576 RVLAVERYLKDQQLGIWCGSKLIC 601


```
RESULT 343
Q9QP04 PRELIMINARY; PRT; 802 AA.
AC Q9QP04;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope (Gp160) (Fragment).
GN ENV OR GP160.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=MP411;
RX MEDLINE=99294894; PubMed=10364493;
RA Triques K., Bourgeois A., Saragosti S., Vidal N., Mpoudi-Etong E.,
RA Nziambi N., Apetret C., Ekwangwa M., Delaporte E., Peeters M.;
RT "High diversity of HIV-1 subtype F strains in Central Africa.";
RL Virology 259:99-109(1999).
DR EMBL; AJ237804; CAB44055.2;
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON TER 1
FT NON TER 802
SQ SEQUENCE 802 AA; 90885 MW; DB27A3076DACC194 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 802;
Best Local Similarity 96.2%; Pred. No. 1.4e-12;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGICGSKGLIC 26
Db 535 RVLAVERYLKDQQLGICGSKGLIC 560

RESULT 344
Q76121 PRELIMINARY; PRT; 807 AA.
AC Q76121;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94103665; PubMed=8277197;
RA Mascola J.J., Louwaghe J.J., McCutchan F.E., Fischer C.L.,
RA Hegerich P.A., Wagner K.F., Fowler A.K., McNeil J.G., Burke D.S.;
RT "Two antigenically distinct subtypes of human immunodeficiency virus
RT type 1: viral genotype predicts neutralization serotype.";
RL J. Infect. Dis. 169:48-54(1993).
DR EMBL; L14570; AAA3875.1;
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
```

```
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON TER 1
FT NON TER 807
SQ SEQUENCE 807 AA; 91339 MW; EA982966E4C41F70 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 807;
Best Local Similarity 96.2%; Pred. No. 1.4e-12;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGICGSKGLIC 26
Db 534 RVLAVERYLKDQQLGICGSKGLIC 559

RESULT 345
O41530 PRELIMINARY; PRT; 813 AA.
AC O41530;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C06;
RX MEDLINE=98105804; PubMed=9445059;
RA Connor R.I., Korber B.T.M., Graham B.S., Hahn B.H., Ho D.D.,
RA Walker B.D., Neumann A.U., Vermond S.H., Meatecky J., Jackson S.,
RA Penmore E., Cao Y., Gao F., Kalams S., Kunstman K.J., McDonald D.,
RA McWilliams N., Trkola A., Moore J.P., Wolinsky S.M.;
RT "Immunological and virological analyses of persons infected by human
RT immunodeficiency virus type 1 while participating in trials of
RT recombinant gp120 subunit vaccines.";
RL J. Virol. 72:1552-1576(1998).
DR EMBL; U84794; AAC58818.1;
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR InterPro; IPR005829; Sug_transporter.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
DR PROSITE; PS00216; SUGAR_TRANSPORT_1; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON TER 1
FT NON TER 813 AA; 91793 MW; AD69BB84A48FC968 CRC64;

Query Match 99.3%; Score 138; DB 15; Length 813;
Best Local Similarity 96.2%; Pred. No. 1.4e-12;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGICGSKGLIC 26
Db 586 RVLAVERYLKDQQLGICGSKGLIC 611

RESULT 346
Q9QSQ7 PRELIMINARY; PRT; 832 AA.
AC Q9QSQ7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein.
GN ENV.
```

```
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=VI850;
RX MEDLINE=20192166; PubMed=10725202;
RA Laakkonen T., Carr J.K., Janssens W., Liitsola K., Gotte D.,
RA McCutchan F.E., Op de Coul E., Cornelissen M., Heyndrickx L.,
RA van der Groen G., Salminen M.O.;
RT "Virtually full-length subtype F and F/D recombinant HIV-1 from Africa
RL and South America.";
RN Virology 269:95-104(2000).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=VI850;
RA Carr J.K., Kim B., Sanders-Buell E., Salminen M.O., Alaeus A.,
RA Albert J.A., Birk D.L., McCutchan F.E.;
RT "HIV-1 isolate VI850 from Zaire, complete genome.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF077336; AAD46094.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
SQ SEQUENCE 832 AA; 93809 MW; 4CE00FD6D9DE269B CRC64;

Query Match          99.3%; Score 138; DB 15; Length 832;
Best Local Similarity 96.2%; Pred. NO. 1.4e-12;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSGKLC 26
DB 555 RVLAVERYLKDQQLGIWCGSGKLC 580

RESULT 347
Q76074 ID Q76074 PRELIMINARY; PRT; 835 AA.
AC Q76074;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=BK132;
RX MEDLINE=93143998; PubMed=1489577;
RA McCutchan F.E., Hegerich P.A., Brennan T.P., Phanuphak P.,
RA Singharaj P., Jungsue A., Berman P.W., Gray A.M., Fowler A.K.,
RA Burke D.S.;
RT "Genetic variants of HIV-1 in Thailand.";
RL AIDS Res. Hum. Retroviruses 8:1887-1895(1992).
DR EMBL; L03697; AAA81527.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 835

SQ SEQUENCE 835 AA; 94918 MW; 46E3566D8B90C92D6 CRC64;
Query Match          99.3%; Score 138; DB 15; Length 835;
Best Local Similarity 96.2%; Pred. NO. 1.4e-12;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSGKLC 26
DB 560 RVLAVERYLKDQQLGIWCGSGKLC 585

RESULT 348
Q8JDN0 ID Q8JDN0 PRELIMINARY; PRT; 837 AA.
AC Q8JDN0;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein.
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]_
RP SEQUENCE FROM N.A.
RX MEDLINE=22032414; PubMed=12036486;
RA Long E.M., Rainwater S.M., Lavreys L., Mandaliya K., Overbaugh J.;
RT "HIV Type 1 Variants Transmitted to Women in Kenya Require the CCR5
RT Coreceptor for Entry, Regardless of the Genetic Complexity of the
RT Infecting Virus.";
RL AIDS Res. Hum. Retroviruses 18:567-576(2002).
DR EMBL; AF407149; AAM66199.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
SQ SEQUENCE 837 AA; 94842 MW; FOCC4026DF90107 CRC64;

Query Match          99.3%; Score 138; DB 15; Length 837;
Best Local Similarity 96.2%; Pred. NO. 1.4e-12;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSGKLC 26
DB 560 RVLAVERYLKDQQLGIWCGSGKLC 585

RESULT 349
Q8JDM6 ID Q8JDM6 PRELIMINARY; PRT; 837 AA.
AC Q8JDM6;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein.
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]_
RP SEQUENCE FROM N.A.
RX MEDLINE=22032414; PubMed=12036486;
RA Long E.M., Rainwater S.M., Lavreys L., Mandaliya K., Overbaugh J.;
RT "HIV Type 1 Variants Transmitted to Women in Kenya Require the CCR5
RT Coreceptor for Entry, Regardless of the Genetic Complexity of the
RT Infecting Virus.";
RL AIDS Res. Hum. Retroviruses 18:567-576(2002).
DR EMBL; AF407149; AAM66199.1; -.
FT
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DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
SQ SEQUENCE 837 AA; 94748 MW; 60B366124081226F CRC64;

Query Match 99.3%; Score 138; DB 15; Length 837;
Best Local Similarity 96.2%; Pred. No. 1.4e-12;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLC 26
|:|||||
Db 560 RVLAVERYLKDQQLGIWGCSGKLC 585

RESULT 350

Q9Q6V0
ID Q9Q6V0 PRELIMINARY; PRT; 838 AA.
AC Q9Q6V0;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Envelope glycoprotein.
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RU98001;
RX MEDLINE=20386750; PubMed=109333619;
RA Liitsola K., Holm K., Bobkov A., Pokrovski V., Smolekaja T.,
R Leinikki P., Osmannov S., Salminen M., UNAIDS Virus Isolation Network;
RT "An AB recombinant and its parental HIV type 1 strains in the area of
the former soviet union: low requirements for sequence identity in
recombination".
RL AIDS Res. Hum. Retroviruses 16:1047-1053(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=RU98001;
RA Liitsola K.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF193277; AAF22333.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
SQ SEQUENCE 838 AA; 95247 MW; 127128F8F5D1F86B CRC64;

Query Match 99.3%; Score 138; DB 15; Length 838;
Best Local Similarity 96.2%; Pred. No. 1.4e-12;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLC 26
|:|||||
Db 561 RVLAVERYLKDQQLGIWGCSGKLC 586

Search completed: May 3, 2004, 06:27:53
Job time : 127 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 3, 2004, 06:21:53 ; Search time 24 Seconds
(without alignments)
56.409 Million cell updates/sec

Title: US-09-733-239-1
Perfect score: 139
Sequence: 1 RILAVERYLKDQQLLGWCSGKLIC 26

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 53

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 50%
Maximum Match 100%
Listing first 500 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	139	100.0	851	1 ENV_HV1B8	P04582 human immun
2	139	100.0	853	1 ENV_HV1MP	P19551 human immun
3	139	100.0	853	1 ENV_HV1Z6	P12487 human immun
4	139	100.0	855	1 ENV_HV1Z6	P04580 human immun
5	139	100.0	856	1 ENV_HV1B1	P03375 human immun
6	139	100.0	856	1 ENV_HV1H2	P04578 human immun
7	139	100.0	856	1 ENV_HV1LW	P04626 human immun
8	139	100.0	856	1 ENV_HV1PV	P03376 human immun
9	139	100.0	861	1 ENV_HV1B8	P03377 human immun
10	139	100.0	867	1 ENV_HV1J3	P12489 human immun
11	138	99.3	847	1 ENV_HV1S1	P19550 human immun
12	138	99.3	852	1 ENV_HV1BN	P12488 human immun
13	138	99.3	855	1 ENV_HV1OY	P20888 human immun
14	137	98.6	856	1 ENV_HV1H3	P04624 human immun
15	137	98.6	856	1 ENV_HV1ZH	P05881 human immun
16	136	97.8	848	1 ENV_HV1JZ	P20871 human immun
17	135	97.1	843	1 ENV_HV1Y2	P35961 human immun
18	135	97.1	847	1 ENV_HV1W2	P05880 human immun
19	135	97.1	852	1 ENV_HV1S3	P19549 human immun
20	135	97.1	855	1 ENV_HV1A2	P03378 human immun
21	135	97.1	856	1 ENV_HV1SC	P05878 human immun
22	135	97.1	856	1 ENV_HV1W1	P31872 human immun
23	135	97.1	865	1 ENV_HV1RH	P04579 human immun
24	135	97.1	868	1 ENV_HV1C4	P05879 human immun
25	134	96.4	856	1 ENV_HV1MN	P05877 human immun
26	132	95.0	853	1 ENV_HV1EL	P04581 human immun
27	132	95.0	861	1 ENV_HV1KB	P18119 human immun
28	125	89.9	846	1 ENV_HV1ND	P18799 human immun
29	125	89.9	863	1 ENV_HV1Z8	P05882 human immun
30	123	88.5	854	1 ENV_SIVCZ	P17281 chimpanzee
31	120	86.3	859	1 ENV_SIVCZ	P04583 human immun
32	84	60.4	380	1 ENV_SIVM2	P08810 simian immu
33	83	59.7	712	1 ENV_HV2S2	P32536 human immun

34	83	59.7	851	1 ENV_HV2D1	P17755 human immun
35	83	59.7	851	1 ENV_HV2G1	P18040 human immun
36	83	59.7	856	1 ENV_HV2N2	P05883 human immun
37	83	59.7	859	1 ENV_HV2CA	P24105 human immun
38	83	59.7	859	1 ENV_HV2D2	P15831 human immun
39	83	59.7	859	1 ENV_HV2ST	P20872 human immun
40	83	59.7	882	1 ENV_SIVM1	P05885 simian immu
41	83	59.7	885	1 ENV_SIVS4	P12492 simian immu
42	83	59.7	889	1 ENV_SIVSP	P19503 simian immu
43	82	59.0	877	1 ENV_SIVAG	P27977 simian immu
44	81	58.3	854	1 ENV_SIVAI	P02837 simian immu
45	81	58.3	865	1 ENV_SIVAT	P05886 simian immu
46	81	58.3	880	1 ENV_SIVML	P11267 simian immu
47	80	57.6	768	1 ENV_SIVAI	P27757 simian immu
48	80	57.6	857	1 ENV_HV2KR	P27757 simian immu
49	80	57.6	881	1 ENV_SIVMK	P05884 simian immu
50	79	56.8	821	1 ENV_SIVGB	P22380 simian immu
51	79	56.8	858	1 ENV_HV2RO	P04577 human immun
52	77	55.4	846	1 ENV_HV2SB	P12449 human immun
53	76	54.7	860	1 ENV_HV2BE	P18094 human immun

ALIGNMENTS

RESULT 1

ENV_HV1B8	STANDARD;	PRT;	851 AA.
AC	P04582;		
DT	13-AUG-1987 (Rel. 05, Created)		
DT	13-AUG-1987 (Rel. 05, Last sequence update)		
DT	10-OCT-2003 (Rel. 42, Last annotation update)		
DE	Envelope polypeptide GP160 precursor [Contains: Exterior membrane		
DE	glycoprotein (GP120); Transmembrane glycoprotein (GP41)].		
GN	ENV.		
OS	Human immunodeficiency virus type 1 (BH8 isolate) (HIV-1).		
OC	Viruses; Retroviral viruses; Retroviridae; Lentivirus.		
OX	NCBI_TaxID=11684;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=85111123; PubMed=2578615;		
RA	Ratner L., Haseltine W., Patarca R., Livak K.J., Starcich B.R.,		
RA	Josephs S.F., Ivanoff L., Rafalski J.A., Whitehorn E.A.,		
RA	Baumeister K., Dorian B.R., Petteway S.R. Jr., Pearson M.L.,		
RA	Lautenberger J.A., Papas T.S., Ghayeb J., Chang N.T., Gallo R.C.,		
RA	Wong-Staal F.J.		
RT	"Complete nucleotide sequence of the AIDS-virus, HTLV-III.";		
RL	Nature 313:277-284 (1985).		
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CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -		
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/		
CC	or send an email to license@isb-sib.ch).		
CC	-----		
CC	EMBL; K02011; AAA44661.1;		
DR	PDB; 1D8H; 13-JAN-99.		
DR	PDB; 1HHG; 31-OCT-93.		
DR	PDB; 1Q03; 02-JAN-00.		
DR	PDB; 1S2T; 24-DEC-97.		
DR	HIV; K02011; ENVSBH8.		
DR	GlycoSuiteDB; P04582;		
DR	InterPro; IPR000328; Env_GP41.		
DR	InterPro; IPR000777; GP120.		
DR	Pfam; PF00516; GP120; 1.		
DR	Pfam; PF00517; GP41; 1.		
KW	AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal;		
KW	3D-structure.		
FT	SIGNAL	1	30
FT	CHAIN	31	506
FT	CHAIN	507	851
FT	EXTERIOR MEMBRANE GLYCOPROTEIN.		
FT	TRANSMEMBRANE GLYCOPROTEIN.		

DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Envelope polyprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (23/CDC-234 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11683;
RN [1]
RP SEQUENCE FROM N.A.
RA Theodore T., Buckler-White A.;
RL Submitted (NOV-1988) to the HIV data bank.
CC -----
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CC -----
CC EMBL; M22639; AAA45370.1; -;
DR PIR; S54384; S54384.
DR HIV; M22639; ENV\$2226.
DR InterPro; IPR000328; Env_GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal.
KW Signal.
FT CHAIN 1 31 BY SIMILARITY.
FT CHAIN 32 508 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 509 853 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 53 73 BY SIMILARITY.
FT DISULFID 118 206 BY SIMILARITY.
FT DISULFID 125 197 BY SIMILARITY.
FT DISULFID 130 154 BY SIMILARITY.
FT DISULFID 219 248 BY SIMILARITY.
FT DISULFID 229 240 BY SIMILARITY.
FT DISULFID 297 330 BY SIMILARITY.
FT DISULFID 376 442 BY SIMILARITY.
FT DISULFID 383 415 BY SIMILARITY.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 137 137 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 153 153 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 157 157 N-LINKED (GLCNAC. .) (POTENTIAL).
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FT CARBOHYD 188 188 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 198 198 N-LINKED (GLCNAC. .) (POTENTIAL).
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FT CARBOHYD 263 263 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 277 277 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 290 290 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 296 296 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 331 331 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 338 338 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 353 353 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 384 384 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 390 390 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 402 402 N-LINKED (GLCNAC. .) (POTENTIAL).
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FT CARBOHYD 608 608 N-LINKED (GLCNAC. .) (POTENTIAL).
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FT CARBOHYD 634 634 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 671 671 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 853 AA; 97043 MW; 849B08CBFAFF7008 CRC64;

Query Match 100.0%; Score 139; DB 1; Length 853;
Best Local Similarity 100.0%; Pred. No. 1.4e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RILAVERYLKQDQLGICGSGKILIC 26
DB 576 RILAVERYLKQDQLGICGSGKILIC 601
RESULT 4
ENV_HV126 STANDARD; PRT; 855 AA.
AC P04580;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope polyprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (Zaire 6 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11708;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87248097; PubMed=3036660;
RA Srinivasan A., Anand R., York D., Ranganathan P., Feorino P.,
RA Schochetman G., Curran J., Kalyanaraman V.S., Luciw P.A.,
RA Sanchez-Pescador R.;
RT "Molecular characterization of human immunodeficiency virus from Zaire: nucleotide sequence analysis identifies conserved and variable domains in the envelope gene."
RT Gene 52:71-82(1987).
CC -----
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CC -----
CC EMBL; K03458; AAA45380.1; -;
DR PIR; D26192; VCLJZR.
DR HIV; K03458; ENV\$26.
DR InterPro; IPR00328; Env_GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal.
FT CHAIN 1 30 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 31 510 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 53 73 BY SIMILARITY.
FT DISULFID 118 207 BY SIMILARITY.
FT DISULFID 125 198 BY SIMILARITY.
FT DISULFID 130 155 BY SIMILARITY.
FT DISULFID 220 249 BY SIMILARITY.
FT DISULFID 230 241 BY SIMILARITY.
FT DISULFID 238 332 BY SIMILARITY.
FT DISULFID 378 444 BY SIMILARITY.
FT DISULFID 395 417 BY SIMILARITY.
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FT CARBOHYD 129 129 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 140 140 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 145 145 N-LINKED (GLCNAC. .) (POTENTIAL).
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FT CARBOHYD 158 158 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 189 189 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 199 199 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 236 236 N-LINKED (GLCNAC. .) (POTENTIAL).


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FT DISULFID 228 239 BY SIMILARITY.
FT DISULFID 296 331 BY SIMILARITY.
FT DISULFID 378 445 BY SIMILARITY.
FT DISULFID 385 418 BY SIMILARITY.
FT CARBOHYD 88 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 136 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 141 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 156 N-LINKED (GLCNAC. .) (POTENTIAL).
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FT CARBOHYD 301 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 332 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 339 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 356 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 366 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 386 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 392 N-LINKED (GLCNAC. .) (POTENTIAL).
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FT CARBOHYD 611 N-LINKED (GLCNAC. .) (POTENTIAL).
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FT CARBOHYD 816 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 856 AA; 96938 MW; 0C2411332CFE76687 CRC64;

Query Match 100.0%; Score 139; DB 1; Length 856;
Best Local Similarity 100.0%; Pred. No. 1.4e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSKGLIC 26
Db 579 RILAVERYLKDQQLGIWCGSKGLIC 604

RESULT 8
ENV_HV1PV
AC P03376; STANDARD; PRT; 856 AA.
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1996 (Rel. 01, Last sequence update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (PV22 isolate) (HIV-1).
OC Viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11700;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85111157; PubMed=2982104;
RA Muesing M.A., Smith D.H., Cabradilla C.D., Benton C.V., Lasky L.A.,
RA Capon D.J..
RT "Nucleic acid structure and expression of the human
RL Nature 313:450-458(1985).
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CC -----
DR EMBL; K02083; AAB59873.1; -.
DR EMBL; X01762; CAA25903.1; ALT_SEQ.
DR PIR; A03974; CLJVL.
DR HIV; K02083; ENVSPV22.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
KW Signal.
FT SIGNAL 1 30
FT CHAIN 31 511 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 512 856 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 54 74 BY SIMILARITY.
FT DISULFID 119 205 BY SIMILARITY.
FT DISULFID 126 196 BY SIMILARITY.
FT DISULFID 131 157 BY SIMILARITY.
FT DISULFID 218 247 BY SIMILARITY.
FT DISULFID 228 239 BY SIMILARITY.
FT DISULFID 296 331 BY SIMILARITY.
FT DISULFID 378 445 BY SIMILARITY.
FT DISULFID 385 418 BY SIMILARITY.
FT CARBOHYD 88 88 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 136 136 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 141 141 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 156 156 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 160 160 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 197 197 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 230 230 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 234 234 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 241 241 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 262 262 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 276 276 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 295 295 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 301 301 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 339 339 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 356 356 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 386 386 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 397 397 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 406 406 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 448 448 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 463 463 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 625 625 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 637 637 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 674 674 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 750 750 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 816 816 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 856 AA; 97339 MW; 5FCDB1DC3C1209B3 CRC64;

Query Match 100.0%; Score 139; DB 1; Length 856;
Best Local Similarity 100.0%; Pred. No. 1.4e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSKGLIC 26
Db 579 RILAVERYLKDQQLGIWCGSKGLIC 604

RESULT 9
ENV_HV1BR
ID ENV_HV1BR STANDARD; PRT; 861 AA.
AC P03377;
DT 21-JUL-1996 (Rel. 01, Created)
DT 21-JUL-1996 (Rel. 01, Last sequence update)
```

10-OCT-2003 (Rel. 42, Last annotation update)
Envelope polyprotein GP160 precursor (Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)).
ENV.
Human immunodeficiency virus type 1 (BRU isolate) (HIV-1).
OS Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11686;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=85099333; PubMed=29816335;
RA Wain-Hobson S., Sonigo P., Danos O., Cole S., Alizon M.;
RT "Nucleotide sequence of the AIDS virus, LAV.";
RL Cell 40:9-17(1985).
CC -----
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CC -----
EMBL; K02013; AAB59751.1; -;
DR EMBL; A04321; CAA00352.1; -;
DR PIR; A03975; VCLJLV.
DR PDB; 1ERF; 20-FEB-02.
DR HIV; K02013; ENV\$BRU.
DR InterPro; IPR000328; Env GP41.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Transmembrane; Signal;
KW 3D-structure.
FT SIGNAL 1 30
FT CHAIN 31 516 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 517 861 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 54 74 BY SIMILARITY.
FT DISULFID 119 210 BY SIMILARITY.
FT DISULFID 126 201 BY SIMILARITY.
FT DISULFID 131 162 BY SIMILARITY.
FT DISULFID 223 252 BY SIMILARITY.
FT DISULFID 233 244 BY SIMILARITY.
FT DISULFID 301 336 BY SIMILARITY.
FT DISULFID 383 450 BY SIMILARITY.
FT DISULFID 390 423 BY SIMILARITY.
FT CARBOHYD 88 98 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 161 161 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 191 191 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 202 202 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 235 235 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 239 239 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 246 246 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 267 267 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 281 281 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 294 294 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 300 300 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 306 306 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 337 337 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 344 344 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 361 361 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 391 391 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 402 402 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 411 411 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 453 453 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 468 468 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 621 621 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 630 630 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 642 642 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 679 679 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 755 755 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 821 821 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 861 AA; 97487 MW; 04DE2B4D4E4FD63A CRC64;
Query Match 100.0%; Score 139; DB 1; Length 861;
Best Local Similarity 100.0%; Pred. No. 1.4e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RILAVERYLKDQQLGIGWCSGKLC 26
Db 584 RILAVERYLKDQQLGIGWCSGKLC 609
RESULT 10
ENV_HVLJ3
ID ENV_HVLJ3 STANDARD; PRT; 867 AA.
AC P12489;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope polyprotein GP160 precursor (Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)).
DE ENV.
OS Human immunodeficiency virus type 1 (JH3 isolate) (HIV-1).
OS Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11694;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89352108; PubMed=2669897;
RA Komiya N., Hattori N., Inoue J., Sakuma S., Kurimura T., Yoshida M.;
RT "Nucleotide sequences of gag and env genes of a Japanese isolate of HIV-1 and their expression in bacteria.";
RL AIDS Res. Hum. Retroviruses 5:411-419(1989).
CC -----
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CC -----
EMBL; M21138; AAB03526.1; -;
DR HIV; M21138; ENV\$JH3
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
KW Signal.
FT SIGNAL 1 30 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 31 516 TRANSMEMBRANE GLYCOPROTEIN.
FT CHAIN 517 867 BY SIMILARITY.
FT DISULFID 53 73 BY SIMILARITY.
FT DISULFID 118 217 BY SIMILARITY.
FT DISULFID 125 208 BY SIMILARITY.
FT DISULFID 130 160 BY SIMILARITY.
FT DISULFID 230 259 BY SIMILARITY.
FT DISULFID 240 251 BY SIMILARITY.
FT DISULFID 308 342 BY SIMILARITY.
FT DISULFID 388 457 BY SIMILARITY.
FT DISULFID 395 430 BY SIMILARITY.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 143 143 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 159 159 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 163 163 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 189 189 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 199 199 N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT CARBOHYD 209 209 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 246 246 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 253 253 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 274 274 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 288 288 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 307 307 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 350 350 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 366 366 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 372 372 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 396 396 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 402 402 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 408 408 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 412 412 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 418 418 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 423 423 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 460 460 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 475 475 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 622 622 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 627 627 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 636 636 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 648 648 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 867 AA; 98399 MW; 5F23101468B8E8680 CRC64;

Query Match 100.0%; Score 139; DB 1; Length 867;
Best Local Similarity 100.0%; Pred. No. 1.5e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSKGLIC 26
Db 590 RILAVERYLKDQQLGIWCGSKGLIC 615

RESULT 11
ENV_HV1S1
ID ENV_HV1S1 STANDARD; PRT; 847 AA.
AC F19550;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (SF162 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11691;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90347835; PubMed=2384920;
RA Cheng-Wayer C., Quiroga M., Tung J.W., Dina D., Levy J.;
RT "Viral determinants of human immunodeficiency virus type 1 T-cell or
macrophage tropism, cytopathogenicity, and CD4 antigen modulation.";
RL J. Virol. 64:4390-4398(1990).
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entities requires a license agreement (see http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
DR EMBL; M65024; AAA45072.1; .
DR PDB; 10BE; 15-MAY-97.
DR HIV; M38428; ENV5SF162.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP20.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal;
KW 3D-structure.
FT SIGNAL 1 29
FT CHAIN 30 502 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 503 847 TRANSMEMBRANE GLYCOPROTEIN.
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FT DISULFID 53 73 BY SIMILARITY.
FT DISULFID 118 203 BY SIMILARITY.
FT DISULFID 125 194 BY SIMILARITY.
FT DISULFID 130 155 BY SIMILARITY.
FT DISULFID 216 245 BY SIMILARITY.
FT DISULFID 226 237 BY SIMILARITY.
FT DISULFID 294 328 BY SIMILARITY.
FT DISULFID 374 435 BY SIMILARITY.
FT DISULFID 381 408 BY SIMILARITY.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 135 135 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 154 154 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 195 195 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 232 232 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 239 239 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 260 260 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 274 274 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 299 299 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 329 329 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 336 336 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 352 352 N-LINKED (GLCNAC. .) (POTENTIAL).
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FT CARBOHYD 392 392 N-LINKED (GLCNAC. .) (POTENTIAL).
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FT CARBOHYD 401 401 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 438 438 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 454 454 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 602 602 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 607 607 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 628 628 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 847 AA; 96135 MW; 0A901317FD7FF2AB CRC64;

Query Match 99.3%; Score 138; DB 1; Length 847;
Best Local Similarity 96.2%; Pred. No. 2e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSKGLIC 26
Db 570 RILAVERYLKDQQLGIWCGSKGLIC 595

RESULT 12
ENV_HV1EN
ID ENV_HV1EN STANDARD; PRT; 852 AA.
AC P12488;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (1BR isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11693;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89085613; PubMed=2789516;
RA Anand R., Thayer R., Srinivasan A., Nayyar S., Gardner M., Luciw P.,
RA Dandekar S.;
RT "Biological and molecular characterization of human immunodeficiency
virus (HIV-1BR) from the brain of a patient with progressive
dementia.";
RL Virology 168:79-89(1989).
CC -1- MISCELLANEOUS: THIS VIRUS IS CYTOPATHICALLY ACTIVE AND WAS
HARVESTED FROM THE BRAIN TISSUE OF A NEUROLOGICAL AIDS PATIENT.
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CC -----
 DR EMBL; M21098; AAA44221.1; -;
 DR PIR; A31667; VCLJBR.
 DR PDB; 1IM7; 23-OCT-02.
 DR HIV; M21098; ENV\$BRVA.
 DR InterPro; IPR000328; Env GP41.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 DR AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal;
 KW 3D-structure.
 FT SIGNAL 1 30

FT CHAIN 31 507 EXTERIOR MEMBRANE GLYCOPROTEIN.
 FT CHAIN 508 852 TRANSMEMBRANE GLYCOPROTEIN.
 FT DISULFID 54 74 BY SIMILARITY.
 FT DISULFID 119 205 BY SIMILARITY.
 FT DISULFID 126 196 BY SIMILARITY.
 FT DISULFID 131 155 BY SIMILARITY.
 FT DISULFID 218 247 BY SIMILARITY.
 FT DISULFID 228 238 BY SIMILARITY.
 FT DISULFID 296 330 BY SIMILARITY.
 FT DISULFID 376 439 BY SIMILARITY.
 FT DISULFID 383 412 BY SIMILARITY.
 FT CARBOHYD 49 49 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 88 88 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 135 135 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 138 138 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 154 154 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 158 158 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 197 197 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 234 234 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 241 241 N-LINKED (GLCNAC. .) (POTENTIAL).
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 FT CARBOHYD 276 276 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 289 289 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 295 295 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 301 301 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 331 331 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 354 354 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 360 360 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 384 384 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 390 390 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 396 396 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 400 400 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 442 442 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 456 456 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 607 607 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 612 612 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 621 621 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 633 633 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 670 670 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 812 812 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 852 AA; 97203 MW; 2BB866345DEC915F CRC64;

Query Match 99.3%; Score 138; DB 1; Length 852;
 Best Local Similarity 96.2%; Pred. No. 2e-13;

Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RILAVERYLKDQQLGWCCKGLIC 26

Db 575 RVLAVERYLKDQQLGWCCKGLIC 600

RESULT 13

ENV HV10Y

ID ENV HV10Y STANDARD; PRT; 855 AA.

AC P20888;

DT 01-FEB-1991 (Rel. 17, Created)

DT 01-FEB-1991 (Rel. 17, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Envelope polyprotein GP160 precursor [Contains: Exterior membrane
 DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (OVI isolate) (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX MCBV_taxid=11699;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90148544; PubMed=2559749;
 RA Huet T., Dazza M.C., Brun-Vezinet F., Roelants G.E., Main-Hobson S.;
 RT "A highly defective HIV-1 strain isolated from a healthy Gabonese
 RT individual presenting an atypical western blot.";
 RL AIDS 3:707-715(1989).
 CC -1- MISCELLANEOUS: THE OVI ISOLATE WAS TAKEN FROM THE BLOOD OF A
 CC HEALTHY GABONESE INDIVIDUAL.
 CC -----
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DR EMBL; M26727; AA83397.1; -;
 DR HIV; M26727; ENV\$OVI.
 DR InterPro; IPR000328; Env GP41.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
 KW SIGNAL.
 FT SIGNAL 1 29
 FT CHAIN 30 509 EXTERIOR MEMBRANE GLYCOPROTEIN.
 FT CHAIN 510 855 TRANSMEMBRANE GLYCOPROTEIN.
 FT DISULFID 53 73 BY SIMILARITY.
 FT DISULFID 118 210 BY SIMILARITY.
 FT DISULFID 125 201 BY SIMILARITY.
 FT DISULFID 130 162 BY SIMILARITY.
 FT DISULFID 223 252 BY SIMILARITY.
 FT DISULFID 233 244 BY SIMILARITY.
 FT DISULFID 301 335 BY SIMILARITY.
 FT DISULFID 381 442 BY SIMILARITY.
 FT DISULFID 398 415 BY SIMILARITY.
 FT CARBOHYD 87 87 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 134 134 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 142 142 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 145 145 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 161 161 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 165 165 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 192 192 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 202 202 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 239 239 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 246 246 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 267 267 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 281 281 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 294 294 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 300 300 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 306 306 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 336 336 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 359 359 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 389 389 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 395 395 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 399 399 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 405 405 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 458 458 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 610 610 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 615 615 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 624 624 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 636 636 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 815 815 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 855 AA; 97476 MW; 9CF82A607ADD62DA CRC64;

Query Match 99.3%; Score 138; DB 1; Length 855;
 Best Local Similarity 96.2%; Pred. No. 2e-13;
 Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSGKLC 26
 :|||||:|||||:|||||:|||||:
 Db 578 RVLAVERYLKDQQLGIWCGSGKLC 603

RESULT 14
 ENV_HV1H3
 ID ENV_HV1H3 STANDARD; PRT; 856 AA.
 AC P04624;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DE 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
 glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (HXB3 isolate) (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11707;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85228248; PubMed=2988795;
 RA Crowl R., Ganguly K., Gordon M., Conroy R., Schaber M., Kramer R.,
 RA Shaw G.M., Wong-Staal F., Reddy E.P.;
 RT "HTLV-III env gene products synthesized in E. coli are recognized by
 antibodies present in the sera of AIDS patients.";
 RL Cell 41:979-986(1985).

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CC EMBL; M14100; AAA44679.1; -.
 DR PDB; 1JAU; 17-OCT-01.
 DR PDB; 1JAV; 17-OCT-01.
 DR HIV; M14100; ENVSHXB3.
 DR InterPro; IPR000328; Env GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 DR AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal;
 KW 3D-structure.

FT SIGNAL 1 30
 FT CHAIN 31 511
 FT CHAIN 512 856
 FT DISULFID 119 205
 FT DISULFID 126 196
 FT DISULFID 131 157
 FT DISULFID 218 247
 FT DISULFID 228 239
 FT DISULFID 236 331
 FT DISULFID 378 445
 FT DISULFID 385 418
 FT CARBOHYD 88 88
 FT CARBOHYD 136 136
 FT CARBOHYD 141 141
 FT CARBOHYD 156 156
 FT CARBOHYD 160 160
 FT CARBOHYD 186 186
 FT CARBOHYD 197 197
 FT CARBOHYD 230 230
 FT CARBOHYD 234 234
 FT CARBOHYD 241 241
 FT CARBOHYD 262 262
 FT CARBOHYD 276 276

N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 624 624 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 750 750 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 856 AA; 97188 MW; 3373C68BB84C1AFC CRC64;

Query Match 98.6%; Score 137; DB 1; Length 856;
 Best Local Similarity 96.2%; Pred. No. 2.9e-13;
 Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSGKLC 26
 :|||||:|||||:|||||:|||||:
 Db 579 RILAVERYLKDQQLGIWCGSGKLC 604

RESULT 15

ENV_HV1ZH
 ID ENV_HV1ZH STANDARD; PRT; 856 AA.
 AC P05881;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Envelope polyprotein GP160 precursor [Contains: Exterior membrane
 glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (Zaire H2321 isolate) (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11692;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89228766; PubMed=2713163;
 RA Srinivasan A., York D., Butler D. Jr., Jannoun-Nasr R., Getchell J.,
 RA McCormick J., Ou C.Y., Myers G., Smith T., Chen E.;
 RT "Molecular characterization of HIV-1 isolated from a serum collected
 RT in 1976: nucleotide sequence comparison to recent isolates and
 RT generation of hybrid HIV."
 RL AIDS Res. Hum. Retroviruses 5:121-129(1989).
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CC EMBL; M15896; AAB53948.1; -.
 DR PIR; A44963; A44963.
 DR HIV; M15896; ENVZ321.
 DR InterPro; IPR000328; Env GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
 Signal.
 FT SIGNAL 1 29
 FT CHAIN 30 511
 FT CHAIN 512 856
 FT CHAIN 512 856

EXTERIOR MEMBRANE GLYCOPROTEIN.
 TRANSMEMBRANE GLYCOPROTEIN.

FT DISULFID 53 73 BY SIMILARITY. (POTENTIAL).
FT DISULFID 118 206 BY SIMILARITY. (POTENTIAL).
FT DISULFID 125 197 BY SIMILARITY. (POTENTIAL).
FT DISULFID 130 153 BY SIMILARITY. (POTENTIAL).
FT DISULFID 219 248 BY SIMILARITY. (POTENTIAL).
FT DISULFID 229 240 BY SIMILARITY. (POTENTIAL).
FT DISULFID 297 331 BY SIMILARITY. (POTENTIAL).
FT DISULFID 379 445 BY SIMILARITY. (POTENTIAL).
FT DISULFID 386 418 BY SIMILARITY. (POTENTIAL).
FT CARBOHYD 87 87 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 132 132 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 138 138 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 152 152 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 156 156 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 183 183 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 198 198 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 242 242 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 263 263 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 277 277 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 294 294 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 302 302 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 339 339 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 355 355 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 364 364 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 387 387 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 393 393 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 402 402 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 411 411 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 448 448 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 461 461 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 462 462 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 465 465 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 637 637 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 856 AA; 96909 MW; 8396E3F8BBD174E CRC64;
Query Match 98.6%; Score 137; DB 1; Length 856;
Best Local Similarity 96.2%; Pred. No. 2.9e-13; Indels 0; Gaps 0;
Matches 25; Conservative 1; Mismatches 0;
QY 1 RILAVERYLKDQQLGWCSGKLC 26
|||||
Db 579 RILAVERYLKDQQLGWCSGKLC 604
|||||
RESULT 16
ENV_HV1JR
ID ENV_HV1JR STANDARD; PRT; 848 AA.
AC P20871;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (JRCSF isolate) (HIV-1).
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11688;
RN [1]
RP SEQUENCE FROM N.A.
RA Koyanagi S., Chen I.S.Y.;
RL Submitted (DEC-1988) to the HIV data bank.
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CC EMBL; M38429; AAB03749.1; -.
DR PDB; 1CE4; 18-MAR-99.
DR HIV; M38429; ENVJRCSE.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal;
3D-structure.
FT SIGNAL 1 32 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 33 503 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 53 73 BY SIMILARITY.
FT DISULFID 118 203 BY SIMILARITY.
FT DISULFID 125 194 BY SIMILARITY.
FT DISULFID 130 154 BY SIMILARITY.
FT DISULFID 216 245 BY SIMILARITY.
FT DISULFID 226 237 BY SIMILARITY.
FT DISULFID 294 328 BY SIMILARITY.
FT DISULFID 374 437 BY SIMILARITY.
FT DISULFID 381 410 BY SIMILARITY.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 134 134 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 137 137 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 153 153 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 157 157 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 185 185 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 195 195 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 228 228 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 239 239 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 260 260 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 274 274 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 287 287 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 299 299 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 329 329 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 336 336 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 352 352 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 382 382 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 388 388 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 403 403 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 440 440 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 453 453 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 603 603 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 608 608 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 617 617 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 629 629 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 808 808 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 848 AA; 96475 MW; 20767F51227EC3F3 CRC64;
Query Match 97.8%; Score 136; DB 1; Length 848;
Best Local Similarity 92.3%; Pred. No. 4.1e-13;
Matches 24; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 RILAVERYLKDQQLGWCSGKLC 26
|:|||||
Db 571 RVLAVERYLKDQQLGWCSGKLC 596
|:|||||
RESULT 17
ENV_HV1Y2
ID ENV_HV1Y2 STANDARD; PRT; 843 AA.
AC P35961;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Envelope polyprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (YU-2 isolate) (HIV-1).
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.

	FT	DISULFID	229	240	BY SIMILARITY.
	FT	DISULFID	237	331	BY SIMILARITY.
	FT	DISULFID	337	439	BY SIMILARITY.
	FT	DISULFID	384	412	BY SIMILARITY.
	FT	CARBOHYD	87	87	N-LINKED (GLCNAC..)
	FT	CARBOHYD	129	129	N-LINKED (GLCNAC..)
	FT	CARBOHYD	136	136	N-LINKED (GLCNAC..)
	FT	CARBOHYD	141	141	N-LINKED (GLCNAC..)
	FT	CARBOHYD	142	142	N-LINKED (GLCNAC..)
	FT	CARBOHYD	155	155	N-LINKED (GLCNAC..)
	FT	CARBOHYD	159	159	N-LINKED (GLCNAC..)
	FT	CARBOHYD	189	189	N-LINKED (GLCNAC..)
	FT	CARBOHYD	198	198	N-LINKED (GLCNAC..)
	FT	CARBOHYD	242	242	N-LINKED (GLCNAC..)
	FT	CARBOHYD	263	263	N-LINKED (GLCNAC..)
	FT	CARBOHYD	277	277	N-LINKED (GLCNAC..)
	FT	CARBOHYD	290	290	N-LINKED (GLCNAC..)
	FT	CARBOHYD	296	296	N-LINKED (GLCNAC..)
	FT	CARBOHYD	332	332	N-LINKED (GLCNAC..)
	FT	CARBOHYD	339	339	N-LINKED (GLCNAC..)
	FT	CARBOHYD	355	355	N-LINKED (GLCNAC..)
	FT	CARBOHYD	385	385	N-LINKED (GLCNAC..)
	FT	CARBOHYD	391	391	N-LINKED (GLCNAC..)
	FT	CARBOHYD	397	397	N-LINKED (GLCNAC..)
	FT	CARBOHYD	401	401	N-LINKED (GLCNAC..)
	FT	CARBOHYD	405	405	N-LINKED (GLCNAC..)
	FT	CARBOHYD	442	442	N-LINKED (GLCNAC..)
	FT	CARBOHYD	457	457	N-LINKED (GLCNAC..)
	FT	CARBOHYD	607	607	N-LINKED (GLCNAC..)
	FT	CARBOHYD	612	612	N-LINKED (GLCNAC..)
	FT	CARBOHYD	621	621	N-LINKED (GLCNAC..)
	FT	CARBOHYD	633	633	N-LINKED (GLCNAC..)
	FT	CARBOHYD	812	812	N-LINKED (GLCNAC..)
	SQ	SEQUENCE	852 AA; 96663 MW;	EETBFBP23C9910D CRC64;	(POTENTIAL).
OY			Query Match	97.1%; Score 135; DB 1; Length 852;	
DDB			Best Local Similarity	92.3%; Pred. No. 6e-13;	
			Matches 24; Conservative	2; Mismatches 0; Indels 0; Gaps 0;	
			1 RILAVERYLKDOQLLGWCSGKLIC 26		
			: : :		
			575 RVLAVERYLRDQLLGWCSGKLIC 600		
RESULT 20					
ENV_HVIA2	ID ENV HVIA2	STANDARD; PRT; 855 AA.			
RAC	P03378;				
DT	21-JUL-1986 (Rel. 01, Created)				
DDT	21-JUL-1986 (Rel. 01, Last sequence update)				
DDT	15-JUL-1999 (Rel. 38, Last annotation update)				
DE	Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)]].				
OS	Human immunodeficiency virus type 1 (ARV2/SF2 isolate) (HIV-1). Viruses; Retroid viruses; Retroviridae; Lentivirus.				
XO	[1]_TaxId=11685;				
ERN	NCBI_TaxId=11685;				
RRP	SEQUENCE FROM N.A.				
RXX	MEDLINE=8509453; PubMed=2578227;				
RAA	Sanches-Pescador R., Power M.D., Barr P.J., Steimer K.S., Stempien M.M., Brown-Shmer S.L., Gee W.W., Renard A., Randolph A., Levy J.A., Dina D., Lucivi P.A.;				
FRT	"Nucleotide sequence and expression of an AIDS-associated retrovirus (ARV-2).";				
CC	Science 227:494-492(1985).				
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CC -----
CC EMBL; K02007; AAB59882.1; -.
CC DR HIV; A03976; VCLJ22.
CC DR HIV; K02007; ENV5SF2.
CC DR InterPro; IPR000328; Env_GP41.
CC DR InterPro; IPR000777; GP120.
CC DR Pfam; PF00516; GP120; 1.
CC DR Pfam; PF00517; GP41; 1.
CC DR AIDS; Coat protein; Glycoprotein; Transmembrane;
KW Signal.
FT SIGNAL.
FT CHAIN 1 29
FT CHAIN 30 509
FT CHAIN 510 855
FT DISULFID 53 73
FT DISULFID 118 208
FT DISULFID 125 199
FT DISULFID 130 155
FT DISULFID 221 250
FT DISULFID 231 242
FT DISULFID 299 333
FT DISULFID 380 442
FT DISULFID 387 415
FT CARBOHYD 87 87
FT CARBOHYD 129 129
FT CARBOHYD 140 140
FT CARBOHYD 154 154
FT CARBOHYD 158 158
FT CARBOHYD 184 184
FT CARBOHYD 190 190
FT CARBOHYD 200 200
FT CARBOHYD 223 233
FT CARBOHYD 244 244
FT CARBOHYD 265 265
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FT CARBOHYD 292 292
FT CARBOHYD 298 298
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FT CARBOHYD 334 334
FT CARBOHYD 341 341
FT CARBOHYD 358 358
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FT CARBOHYD 388 388
FT CARBOHYD 394 394
FT CARBOHYD 400 400
FT CARBOHYD 445 445
FT CARBOHYD 458 458
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FT CARBOHYD 610 610
FT CARBOHYD 615 615
FT CARBOHYD 624 624
FT CARBOHYD 636 636
FT CARBOHYD 815 815
SQ SEQUENCE 855 AA; 97438 MW; A38C20573AAC41A2 CRC64;

Query Match 97.1%; Score 135; DB 1; Length 855;
Best Local Similarity 92.3%; Pred. No. 6e-13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLAVRYLKDQQLGIWGCSKGLIC 26
Db 578 RLAVRYLRDQQLGIWGCSKGLIC 603

RESULT 21
ENV_HV1SC STANDARD; PRT; 856 AA.
AC P05878;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope polyprotein GP160 precursor [Contains: Exterior membrane
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DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (SC isolate) (HIV-1).
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_taxid=11702;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88219542; PubMed=3369091;
RA Gurgu C., Guo H.-G., Franchini G., Aldovini A., Collalti E.,
RA Farrell K., Wong-Staal F., Gallo R.C., Reitz M.S. Jr.;
RA "Envelope sequences of two new United States HIV-1 isolates.";
RL Virology 164:531-536(1988).
CC -!- MISCELLANEOUS: THE SC ISOLATE WAS TAKEN FROM AN ARC PATIENT IN
CC 1984 IN SOUTHERN CALIFORNIA.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
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EMBL; M17450; -, NOT ANNOTATED_CDS.

HIV; M17450; ENV5SC.

InterPro; IPR000328; Env GP41.

InterPro; IPR000777; GP120.

Pfam; PF00516; GP120; 1.

Pfam; PF00517; GP41; 1.

AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;

Signal.

FT SIGNAL. 1 29

FT CHAIN 30 510

FT CHAIN 511 856

FT SITE 760 760

FT DISULFID 53 73

FT DISULFID 118 206

FT DISULFID 125 197

FT DISULFID 130 160

FT DISULFID 219 247

FT DISULFID 228 239

FT DISULFID 296 330

FT DISULFID 376 439

FT DISULFID 383 412

FT DISULFID 87 87

FT CARBOHYD 129 129

FT CARBOHYD 135 135

FT CARBOHYD 140 140

FT CARBOHYD 143 143

FT CARBOHYD 159 159

FT CARBOHYD 163 163

FT CARBOHYD 189 189

FT CARBOHYD 198 198

FT CARBOHYD 234 234

FT CARBOHYD 241 241

FT CARBOHYD 262 262

FT CARBOHYD 276 276

FT CARBOHYD 295 295

FT CARBOHYD 301 301

FT CARBOHYD 302 302

FT CARBOHYD 331 331

FT CARBOHYD 338 338

FT CARBOHYD 354 354

FT CARBOHYD 360 360

FT CARBOHYD 384 384

FT CARBOHYD 394 394

FT CARBOHYD 400 400

FT CARBOHYD 405 405

FT CARBOHYD 442 442

FT CARBOHYD 457 457

FT CARBOHYD 611 611

FT CARBOHYD 616 616

FT CARBOHYD 625 625

EXTERIOR MEMBRANE GLYCOPROTEIN.

TRANSMEMBRANE GLYCOPROTEIN.

IN-FRAME TERMINATION CODON.

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FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 856 AA; 97055 MW; DAF4DA600BEA7A08 CRC64;

Query Match. 97.1%; Score 135; DB 1; Length 856;
Best Local Similarity 92.3%; Pred. No. 6e-13; 0; Indels 0; Gaps 0;
Matches 24; Conservative 2; Mismatches 0;

QY 1 RILAVERYLKDQQLGWCCKLIC 26
|:|||||:|||||:|||||:|||||:
Db 579 RVLAVERYLRDQQLGWCCKLIC 604

RESULT 22
ENV HV1W1 STANDARD; PRT; 856 AA.
AC P31872;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Envelope polyprotein GP160 precursor [Contains: Exterior membrane
DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (WMJ1 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=31678;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86218077; PubMed=2423250;
RA Starcich B.R., Hahn B.H., Shaw G.M., McNeely P.D., Modrow S., Wolf H.,
RA Parks E.S., Parks W.P., Josephs S.F., Gallo R.C., Wong-Staal F.;
RT "Identification and characterization of conserved and variable
RT regions in the envelope gene of HTLV-III/LAV, the retrovirus of
RT AIDS.";
RL Cell 45:637-648 (1986).
CC -! MISCELLANEOUS: ISOLATES WMJ1, WMJ2, AND WMJ3 WERE OBTAINED FROM
CC BLOOD SAMPLES SEQUENTIALLY TAKEN FROM A TWO-YEAR OLD HAITIAN WHO
CC WAS PERINATALLY INFECTED BY HER MOTHER.
CC
CC PIR; A24774; VCLJ3W.
DR PDB; 1LB0; 04-DEC-02.
DR PDB; 1LCX; 04-DEC-02.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal;
KW 3D-structure. 1 29
FT SIGNAL 1 29
FT CHAIN 30 510 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 511 856 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 53 73 BY SIMILARITY.
FT DISULFID 118 205 BY SIMILARITY.
FT DISULFID 125 196 BY SIMILARITY.
FT DISULFID 130 152 BY SIMILARITY.
FT DISULFID 218 247 BY SIMILARITY.
FT DISULFID 228 239 BY SIMILARITY.
FT DISULFID 296 330 BY SIMILARITY.
FT DISULFID 376 444 BY SIMILARITY.
FT DISULFID 383 417 BY SIMILARITY.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 134 134 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 155 155 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT CARBOHYD 331 331 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 338 338 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 354 354 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 360 360 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 394 394 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 404 404 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 447 447 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 459 459 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 625 625 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 856 AA; 97526 MW; DB68D1B49C404DE9 CRC64;

Query Match 97.1%; Score 135; DB 1; Length 856;
Best Local Similarity 92.3%; Pred. No. 6e-13; 0; Indels 0; Gaps 0;
Matches 24; Conservative 2; Mismatches 0;

QY 1 RILAVERYLKDQQLGWCCKLIC 26
|:|||||:|||||:|||||:|||||:
Db 579 RVLAVERYLRDQQLGWCCKLIC 604

RESULT 23
ENV HV1RH STANDARD; PRT; 865 AA.
AC P04579;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope polyprotein GP160 precursor [Contains: Exterior membrane
DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (RP/HAT isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11701;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86218077; PubMed=2423250;
RA Starcich B.R., Hahn B.H., Shaw G.M., McNeely P.D., Modrow S., Wolf H.,
RA Parks E.S., Parks W.P., Josephs S.F., Gallo R.C., Wong-Staal F.;
RT "Identification and characterization of conserved and variable
RT regions in the envelope gene of HTLV-III/LAV, the retrovirus of
RT AIDS.";
RL Cell 45:637-648 (1986).
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M17451; AAA45057.1; .
CC HIV; M17451; ENVSRF.
CC InterPro; IPR000328; Env GP41.
CC InterPro; IPR000777; GP120.
CC Pfam; PF00516; GP120; 1.
CC Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
KW SIGNAL. 1 29
FT CHAIN 30 519 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 520 865 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 53 73 BY SIMILARITY.
FT DISULFID 118 218 BY SIMILARITY.
FT DISULFID 125 209 BY SIMILARITY.
FT DISULFID 130 157 BY SIMILARITY.
FT DISULFID 231 260 BY SIMILARITY.
FT DISULFID 241 252 BY SIMILARITY.
FT DISULFID 309 343 BY SIMILARITY.

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RESULT 25
ENV_HV1M1  STANDARD; PRT; 856 AA.
AC P05877;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (MN isolate) (HIV-1).
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11696;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88219542; PubMed=3369091;
RA Gurgu C., Guo H.-G., Franchini G., Aldovini A., Collalti E.,
RA Farrell K., Wong-Staal F., Gallo R.C., Reitz M.S. Jr.;
RT "Envelope sequences of two new United States HIV-1 isolates.";
RL Virology 164:531-536(1988).
CC -1- MISCELLANEOUS: THE MN ISOLATE WAS TAKEN FROM A PEDIATRIC AIDS
CC PATIENT IN 1984.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M17449; AAA44857.1; --
DR PDB; 1ACV; 31-JUL-94.
DR PDB; 1F58; 29-DEC-99.
DR PDB; 1N1Z; 25-FEB-03.
DR PDB; 1NJO; 25-FEB-03.
DR HIV; M17449; ENV$MN.
DR InterPro; IPR000328; Env GP41.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal;
KW 3D-structure.
FT SIGNAL 1 29
FT CHAIN 30 513 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 514 856 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 53 73
FT DISULFID 118 210 BY SIMILARITY.
FT DISULFID 125 201 BY SIMILARITY.
FT DISULFID 130 162 BY SIMILARITY.
FT DISULFID 223 252 BY SIMILARITY.
FT DISULFID 233 244 BY SIMILARITY.
FT DISULFID 301 335 BY SIMILARITY.
FT DISULFID 381 445 BY SIMILARITY.
FT DISULFID 388 418 BY SIMILARITY.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 129 129 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 135 135 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 140 140 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 141 141 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 146 146 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 161 161 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 165 165 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 191 191 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 202 202 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 246 246 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 267 267 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 281 281 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 294 294 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 300 300 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 336 336 N-LINKED (GLCNAC. .) (POTENTIAL).
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FT CARBOHYD 343 343 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 359 359 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 365 365 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 395 395 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 401 401 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 405 405 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 406 406 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 413 413 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 448 448 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 465 465 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 612 612 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 617 617 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 626 626 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 638 638 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 816 816 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 856 AA; 97140 MW; D197D809940BE732 CRC64;

Query Match 96.4%; Score 134; DB 1; Length 856;
Best Local Similarity 92.3%; Pred. No. 8.6e-13;
Matches 24; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIMGCSGKLC 26
Db 580 RVLAVERYLKDQQLGIMGCSGKLC 605

RESULT 26
ENV_HV1E1  STANDARD; PRT; 853 AA.
AC P04581;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (ELI isolate) (HIV-1).
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11689;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86245056; PubMed=2424612;
RA Alison M., Wan-Hobson S., Montagnier L., Sonigo P.;
RT "Genetic variability of the AIDS virus: nucleotide sequence analysis
RT of two isolates from African patients.";
RL Cell 46:63-74(1986).
CC
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; K03454; AAA44329.1; --
DR EMBL; A07108; CAA00616.1; --
DR HIV; K03454; ENV$ELI.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
KW SIGNAL 1 31 BY SIMILARITY.
FT CHAIN 32 508 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 509 853 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 53 73 BY SIMILARITY.
FT DISULFID 118 206 BY SIMILARITY.
FT DISULFID 125 197 BY SIMILARITY.
FT DISULFID 130 154 BY SIMILARITY.
FT DISULFID 219 248 BY SIMILARITY.
FT DISULFID 229 240 BY SIMILARITY.
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FT DISULFID 297 330 BY SIMILARITY.
FT DISULFID 376 442 BY SIMILARITY.
FT DISULFID 383 416 BY SIMILARITY.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 129 129 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 137 137 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 143 143 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 153 153 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 157 157 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 183 183 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 188 188 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 198 198 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 235 235 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 242 242 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 263 263 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 277 277 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 290 290 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 331 331 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 353 353 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 384 384 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 390 390 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 394 394 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 400 400 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 405 405 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 406 406 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 411 411 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 445 445 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 458 458 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 459 459 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 462 462 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 608 608 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 613 613 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 622 622 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 634 634 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 853 AA; 96721 MW; F9CD864DAAD0D7A5 CRC64;

Query Match 95.0%; Score 132; DB 1; Length 853;
Best Local Similarity 96.2%; Pred. No. 1.7e-12;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 RILAVERYLKDQQLGIWCGSKGLIC 26
DB 576 RILAVERYLKDQQLGIWCGSKGHIC 601

RESULT 27
ENV_HV1KB STANDARD; PRT; 861 AA.
AC F31819;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor (Contains: Exterior membrane
DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)).
GN ENV.
OS Human immunodeficiency virus type 1 (XB-1 isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=36375;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92351552; PubMed=1322587;
RA Shimizu H., Hasebe F., Tsuchie H., Morikawa S., Ushijima H.,
RA Kitamura T.;
RT "Analysis of a human immunodeficiency virus type 1 isolate carrying a
RT truncated transmembrane glycoprotein.";
RL Virology 189:534-546(1992).
CC -!- MISCELLANEOUS: READTHROUGH OF THE TERMINATOR UAG OCCURS BETWEEN
CC THE CODONS FOR 729-ALA AND 730-ARG.
CC
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-----
EMBL; D12582; BAA02124.1; ALT_SEQ.
PIR; A42995; VCLJKB.
InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
Signal.
FT SIGNAL 1 35 POTENTIAL.
FT CHAIN 36 517 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 518 861 TRANSMEMBRANE GLYCOPROTEIN.
FT TRANSMEM 690 711 POTENTIAL.
FT DISULFID 59 79 BY SIMILARITY.
FT DISULFID 124 212 BY SIMILARITY.
FT DISULFID 131 203 BY SIMILARITY.
FT DISULFID 136 160 BY SIMILARITY.
FT DISULFID 225 254 BY SIMILARITY.
FT DISULFID 235 246 BY SIMILARITY.
FT DISULFID 303 337 BY SIMILARITY.
FT DISULFID 383 446 BY SIMILARITY.
FT DISULFID 390 419 BY SIMILARITY.
FT CARBOHYD 93 93 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 141 141 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 145 145 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 146 146 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 159 159 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 163 163 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 191 191 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 192 192 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 237 237 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 241 241 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 248 248 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 269 269 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 283 283 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 296 296 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 308 308 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 338 338 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 345 345 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 361 361 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 367 367 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 397 397 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 403 403 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 408 408 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 414 414 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 449 449 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 465 465 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 468 468 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 617 617 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 622 622 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 631 631 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 643 643 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 821 821 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 861 AA; 98116 MW; 3C06787658F0C9DA CRC64;

Query Match 95.0%; Score 132; DB 1; Length 861;
Best Local Similarity 88.5%; Pred. No. 1.8e-12;
Matches 23; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 RILAVERYLKDQQLGIWCGSKGLIC 26
DB 585 RILAVERYLKDQQLGIWCGSKGFIC 610

RESULT 28
ENV_HV1ND STANDARD; PRT; 846 AA.
ID ENV_HV1ND
AC P18799;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
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FT CARBOHYD 288 288 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 301 301 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 307 307 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 343 343 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 350 350 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 365 365 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 396 396 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 402 402 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 406 406 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 412 412 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 455 455 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 468 468 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 469 469 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 472 472 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 618 618 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 623 623 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 632 632 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 644 644 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 823 823 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 863 AA; 97743 MW; B729CBSA6FAD1641 CRC64;

Query Match 89.9%; Score 125; DB 1; Length 863;
Best Local Similarity 88.5%; Pred. No. 2.2e-11;
Matches 23; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIGCSGKLIC 26
|:|||||:|||||:|||||:|
Db 586 RVLAVESYLKQDQLGIGCSGKHC 611

RESULT 30
ENV_SIVCZ STANDARD; PRT; 854 AA.
AC P172a1;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane
DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Chimpanzee immunodeficiency virus (SIV(cpz)) (CIV).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11723;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90259077; PubMed=2188136;
RA Huet T., Cheynier R., Meyerhans A., Roelants G., Wain-Hobson S.;
RT "Genetic organization of a chimpanzee lentivirus related to HIV-1.";
RL Nature 345:356-359 (1990).
CC -!- SIMILARITY: STRONG, WITH HIV-1 ENV POLYPEPTIDE.
CC -----
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CC -----
CC EMBL; X52154; CAA36407.1; -
CC PIR; S09990; VCLJSI.
CC HIV; X52154; ENV5CPZ.
CC InterPro; IPR000328; Env GP41.
CC Pfam; PF00516; GP120; 1.
CC Pfam; PF00517; GP41; 1.
CC AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
CC Signal.
CC SIGNAL.
FT SIGNAL 1 30
FT CHAIN 31 500 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 501 854 TRANSMEMBRANE GLYCOPROTEIN.
FT TRANSMEM 501 517 POTENTIAL.
FT TRANSMEM 675 693 POTENTIAL.
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FT TRANSMEM 805 821 POTENTIAL.
FT CARBOHYD 134 134 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 140 140 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 143 143 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 154 154 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 158 158 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 195 195 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 239 239 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 260 260 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 267 267 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 274 274 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 299 299 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 331 331 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 336 336 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 351 351 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 356 356 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 384 384 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 426 426 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 432 432 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 446 446 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 450 450 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 601 601 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 608 608 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 628 628 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 854 AA; 95803 MW; 2E249AFAD4FD9B3 CRC64;

Query Match 88.5%; Score 123; DB 1; Length 854;
Best Local Similarity 76.9%; Pred. No. 4.4e-11;
Matches 20; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIGCSGKLIC 26
|:|||||:|||||:|||||:|
Db 569 RLLAVERYLQDQQLGLWGCSGRAVC 594

RESULT 31
ENV_HVIMA STANDARD; PRT; 859 AA.
AC P04583;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane
DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (MAL isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11697;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86245056; PubMed=2424612;
RA Alizon M., Wain-Hobson S., Montagnier L., Sonigo P.;
RT "Genetic variability of the AIDS virus: nucleotide sequence analysis
RT of two isolates from African patients.";
RL Cell 46:63-74 (1986).
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X04415; CAA28016.1; -
CC PIR; A07116; CAA00623.1; -
CC PIR; T01672; T01672.
CC HIV; K03456; ENV$MAL.
CC InterPro; IPR000328; Env GP41.
CC InterPro; IPR000777; GP120.
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FT CARBOHYD 440 440 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 457 457 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 602 602 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 627 627 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 856 AA; 98665 MW; A93B80A7E2B881D6 CRC64;

Query Match 59.7%; Score 83; DB 1; Length 856;
Best Local Similarity 50.0%; Pred. No. 7.2e-05;
Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy 1 RILAVERYLKDQQLGIWGCCKLIC 26
| : : : : : | : : : : : | : : : : : |
Db 569 RVTAIEKYLKQDLNSWGCAPRQVC 594

RESULT 37
ENV_HV2CA STANDARD; PRT; 859 AA.
AC P24105;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 2 (isolate CAM2) (HIV-2).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11715;
RN SEQUENCE FROM N.A.
RX MEDLINE=91170959; PubMed=2005437;
RT Tristram M., Hill F., Karpas A.;
RT "Nucleotide sequence of a Guinea-Bissau-derived human
immunodeficiency virus type 2 proviral clone (HIV-2CAM2).";
RL J. Gen. Virol. 72:721-724(1991).
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CC -----
DR EMBL; D00835; BAA00716.1; --
DR PIR; F38475; VCLJCT.
DR InterPro; IPR000328; Env GP41.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
KW Signal.
FT SIGNAL 1 20
FT CHAIN 21 502 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 503 859 TRANSMEMBRANE GLYCOPROTEIN.
FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 71 71 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 115 115 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 148 148 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 163 163 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 176 176 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 205 205 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 237 237 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 247 247 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 271 271 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 277 277 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 288 288 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 299 299 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 309 309 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 343 343 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 366 366 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 411 411 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 467 467 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 612 612 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 621 621 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 859 AA; 99018 MW; 6F54913F206B26C3 CRC64;

Query Match 59.7%; Score 83; DB 1; Length 859;
Best Local Similarity 50.0%; Pred. No. 7.2e-05;
Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy 1 RILAVERYLKDQQLGIWGCCKLIC 26
| : : : : : | : : : : : | : : : : : |
Db 579 RVTAIEKYLKQDLNSWGCAPRQVC 604

RESULT 38
ENV_HV2D2 STANDARD; PRT; 859 AA.
AC P15831;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 2 (isolate D205, 7) (HIV-2).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11716;
RN SEQUENCE FROM N.A.
RX MEDLINE=90081881; PubMed=2594088;
RT Dietrich U., Adamski M., Kreutz R., Seipp A., Kuehn H.,
Ruebbsamen-Waigmann H.;
RT "A highly divergent HIV-2-related isolate.";
RL Nature 342:948-950(1989).
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CC -----
DR EMBL; X61240; CAA43572.1; --
DR PIR; S08442; S08442.
DR PIR; S24571; S24571.
DR HIV; X16109; ENV2D205.
DR InterPro; IPR000328; Env GP41.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
KW Signal.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 503 EXTERIOR MEMBRANE GLYCOPROTEIN (BY
SIMILARITY).
FT CHAIN 504 859 TRANSMEMBRANE GLYCOPROTEIN
(BY SIMILARITY).
FT CARBOHYD 37 37 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 70 70 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 112 112 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 122 122 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 142 142 N-LINKED (GLCNAC. . .) (POTENTIAL).
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CC EMBL; Y00277; -, NOT_ANNOTATED_CDS.
CC PIR; H28887; VCLJG3.
CC HIV; M16403; ENV$MM142.
CC InterPro; IPR000328; Env GP41.
CC InterPro; IPR000777; GP120.
CC Pfam; PF00516; GP120; 1.
CC Pfam; PF00517; GP41; 1.
CC AIDS; Coat protein; Glycoprotein; Transmembrane;
KW Signal.
FT SIGNAL 1 22
FT CHAIN 23 528
FT CHAIN 529 882
FT SITE 737 737
FT CARBOHYD 37 37
FT CARBOHYD 70 70
FT CARBOHYD 114 114
FT CARBOHYD 149 149
FT CARBOHYD 159 159
FT CARBOHYD 174 174
FT CARBOHYD 187 187
FT CARBOHYD 201 201
FT CARBOHYD 205 205
FT CARBOHYD 215 215
FT CARBOHYD 247 247
FT CARBOHYD 250 250
FT CARBOHYD 257 257
FT CARBOHYD 281 281
FT CARBOHYD 287 287
FT CARBOHYD 298 298
FT CARBOHYD 309 309
FT CARBOHYD 319 319
FT CARBOHYD 374 374
FT CARBOHYD 380 380
FT CARBOHYD 463 463
FT CARBOHYD 474 474
FT CARBOHYD 479 479
FT CARBOHYD 628 628
FT CARBOHYD 637 637
FT CARBOHYD 653 653
FT CARBOHYD 762 762
FT CARBOHYD 882 AA; 101196 MW; 216DD5C08C05DA7 CRC64;
SQ SEQUENCE 882 AA; 101196 MW; 216DD5C08C05DA7 CRC64;

Query Match 59.7%; Score 83; DB 1; Length 882;
Best Local Similarity 50.0%; Pred. No. 7.4e-05;
Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSKLIC 26
Db 595 RVSAIEKYLKDAQQLNANGCAFRQVC 620

RESULT 41
ENV_SIVS4
ID ENV_SIVS4 STANDARD; PRT; 885 AA.
AC P12492;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Simian immunodeficiency virus (F236/smH4 isolate) (sooty mangabey).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11737;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89262053; PubMed=2786147;
RA Hirsch V.M., Olmstead R.A., Murphy-Corb M., Purcell R.H.,
RA Johnson P.R.;
RT "An African primate lentivirus (SIVsm) closely related to HIV-2.";
RL Nature 339:389-392(1989).
RN [2]
RP SEQUENCE FROM N.A.
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CC
CC EMBL; X14307; CAA32487.1; -.
CC PIR; S04322; S04322.
CC HIV; X14307; ENV$MMH4.
CC InterPro; IPR000328; Env GP41.
CC InterPro; IPR000777; GP120.
CC Pfam; PF00516; GP120; 1.
CC Pfam; PF00517; GP41; 1.
CC AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane.
KW CARBOHYD 37 37
FT CARBOHYD 70 70
FT CARBOHYD 114 114
FT CARBOHYD 148 148
FT CARBOHYD 156 156
FT CARBOHYD 173 173
FT CARBOHYD 186 186
FT CARBOHYD 201 201
FT CARBOHYD 213 213
FT CARBOHYD 245 245
FT CARBOHYD 255 255
FT CARBOHYD 279 279
FT CARBOHYD 285 285
FT CARBOHYD 296 296
FT CARBOHYD 307 307
FT CARBOHYD 317 317
FT CARBOHYD 372 372
FT CARBOHYD 378 378
FT CARBOHYD 466 466
FT CARBOHYD 482 482
FT CARBOHYD 485 485
FT CARBOHYD 631 631
FT CARBOHYD 640 640
FT CARBOHYD 656 656
FT CARBOHYD 885 AA; 101863 MW; 7E0D035410D6D988 CRC64;
SQ SEQUENCE 885 AA; 101863 MW; 7E0D035410D6D988 CRC64;

Query Match 59.7%; Score 83; DB 1; Length 885;
Best Local Similarity 50.0%; Pred. No. 7.4e-05;
Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSKLIC 26
Db 598 RVTAIEKYLKDAQQLNSWGCAPRQVC 623

RESULT 42
ENV_SIVSP
ID ENV_SIVSP STANDARD; PRT; 889 AA.
AC P19503;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Simian immunodeficiency virus (PBj14/BCL-3 isolate) (sooty mangabey).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11738;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90272009; PubMed=1971917;
RA Dewhurst S., Embretson J.E., Anderson D.C., Mullins J.I., Fultz P.N.;
RT "Sequence analysis and acute pathogenicity of molecularly cloned
SIVSM-PBj14."
RL Nature 345:636-640(1990).
RN [2]
RP SEQUENCE FROM N.A.
```


FT CARBOHYD 761 761 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 881 AA; 101184 MW; 9052BS4377DD979 CRC64;
Query Match 57.6%; Score 80; DB 1; Length 881;
Best Local Similarity 46.2%; Pred. No. 0.00022;
Matches 12; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIMGCSGKLC 26
ID ENV HV2RO STANDARD; PRT; 821 AA.
AC P22380;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Envelope polyprotein GP160 precursor [Contains: GP120; GP32;
DE Putative protein ENV-EXTN].
GN ENV.
OS Simian immunodeficiency virus (isolate GBI).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11732;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90015168; PubMed=2797181;
RA Tadjimoto H., Hasegawa A., Maki N., Fukasawa M., Miura T., Speidel S.,
RA Cooper R.W., Moriyama E.N., Gojohori T., Hayami M.;
RT "Sequence of a novel simian immunodeficiency virus from a wild-caught
RT African mandrill";
RL Nature 341:539-541(1989).
CC -!- MISCELLANEOUS: THIS IS AN AFRICAN MANDRILL ISOLATE.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M27470; AAB49574.1; -;
DR InterPro; IPR000328; Env GP41.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane.
FT CHAIN 71 71 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 71 98 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 175 175 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 190 190 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 215 215 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 224 224 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 266 266 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 287 287 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 333 333 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 383 383 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 389 389 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 394 394 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 423 423 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 447 447 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 516 516 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 669 669 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 675 675 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 694 694 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 808 808 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 821 AA; 94410 MW; E353367C25CCD095 CRC64;
Query Match 56.8%; Score 79; DB 1; Length 821;
Best Local Similarity 50.0%; Pred. No. 0.00029;

Matches 13; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIMGCSGKLC 26
ID ENV HV2RO STANDARD; PRT; 858 AA.
AC P04577;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Envelope polyprotein GP160 precursor [Contains: Exterior membrane
DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 2 (isolate ROD) (HIV-2).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11720;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87173056; PubMed=3031510;
RA Guyader M., Emerman M., Sonigo P., Clavel F., Montagnier L.,
RA Allison M.;
RT "Genome organization and transactivation of the human
RT immunodeficiency virus type 2";
RL Nature 326:662-669(1987).
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M15390; AAB00770.1; -;
DR EMBL; X05291; CAA28914.1; -;
DR PIR; C26262; VCLJG2.
DR HIV; M15390; ENV52R0D.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
KW Signal.
FT CHAIN 1 17 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 18 501 TRANSMEMBRANE GLYCOPROTEIN.
FT CARBOHYD 34 34 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 67 67 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 76 76 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 119 119 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 120 120 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 166 166 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 179 179 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 192 192 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 193 193 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 196 196 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 206 206 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 248 248 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 272 272 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 278 278 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 300 300 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 310 310 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 367 367 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 371 371 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT CARBOHYD 410 410 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 447 447 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 466 466 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 620 620 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 636 636 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 312 312 T -> I (IN REF. 1; AAB00770).
SQ SEQUENCE 858 AA; 98824 MW; C7266AF1F5C5B9A7 CRC64;

Query Match 56.8%; Score 79; DB 1; Length 858;
Best Local Similarity 46.2%; Pred. No. 0.0003;
Matches 12; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLLGWCSGKLIC 26
| : : : : : |
Db 578 RVTAEIKYLDQARLNSWGCAFRQVC 603

RESULT 52
ENV_HV2SB STANDARD; PRT; 846 AA.
AC P12449;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 2 (isolate SBLISY) (HIV-2).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11718;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89184641; PubMed=2648404;
RA Franchini G., Fargnoli K.A., Giombini F., Jagodzinski L., de Rossi A.,
Bosch M., Biberfeld G., Kenyo A.M., Albert J., Gallo R.C.,
Wong-Staal F.;
RT "Molecular and biological characterization of a replication competent
human immunodeficiency type 2 (HIV-2) proviral clone.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:2433-2437(1989).
CC -----
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CC -----
DR EMBL; J04498; AAB00752.1; -
DR HIV; J04498; ENV$2ISY.
DR InterPro; IPR000328; Env GP41.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
Signal.
FT SIGNAL 1 19
FT CHAIN 20 493 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 494 846 TRANSMEMBRANE GLYCOPROTEIN.
FT CARBOHYD 36 36 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 69 69 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 113 113 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 142 142 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 184 184 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 229 229 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 232 232 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 239 239 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 269 269 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 280 280 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 291 291 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 357 357 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 363 363 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 455 455 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 603 603 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 612 612 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 628 628 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 846 AA; 97693 MW; 3A7B335F914D54C CRC64;

Query Match 55.4%; Score 77; DB 1; Length 846;
Best Local Similarity 46.2%; Pred. No. 0.00061;
Matches 12; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLLGWCSGKLIC 26
| : : : : : |
Db 570 RVTAEIKYLDQARLNSWGCAFRQVC 595

RESULT 53
ENV_HV2BE STANDARD; PRT; 860 AA.
AC P18094;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 2 (isolate BEN) (HIV-2).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11714;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90281594; PubMed=2353457;
RA Kirchhoff F., Jentsch K., Bachmann B., Stuke A., Laloux C.,
Lueke W., Stahl-Henning C., Schneider J., Nieselt K., Eigen M.,
Hunsmann G.;
RT "A novel proviral clone of HIV-2: biological and phylogenetic
relationship to other primate immunodeficiency viruses.";
RL Virology 177:305-311(1990).
CC -!- MISCELLANEOUS: THIS ISOLATE IS FROM A GERMAN AIDS PATIENT (WITH
PREDOMINANTLY NEUROLOGICAL COMPLICATIONS) WHO WAS PROBABLY
INFECTED IN MALI.
CC -----
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CC -----
DR EMBL; M30502; AAB00743.1; -
DR HIV; M30502; ENV$2BEN.
DR InterPro; IPR000328; Env GP41.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
Signal.
FT SIGNAL 1 20
FT CHAIN 21 500 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 501 860 TRANSMEMBRANE GLYCOPROTEIN.
FT CARBOHYD 37 37 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 70 70 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 79 79 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 112 112 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT	CARBOHYD	119	119	N-LINKED	(GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	144	144	N-LINKED	(GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	152	152	N-LINKED	(GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	194	194	N-LINKED	(GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	206	206	N-LINKED	(GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	238	238	N-LINKED	(GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	241	241	N-LINKED	(GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	272	272	N-LINKED	(GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	278	278	N-LINKED	(GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	289	289	N-LINKED	(GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	300	300	N-LINKED	(GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	310	310	N-LINKED	(GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	365	365	N-LINKED	(GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	371	371	N-LINKED	(GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	398	398	N-LINKED	(GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	410	410	N-LINKED	(GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	460	460	N-LINKED	(GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	465	465	N-LINKED	(GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	610	610	N-LINKED	(GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	619	619	N-LINKED	(GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	635	635	N-LINKED	(GLCNAC. . .)	(POTENTIAL).
SQ	SEQUENCE	860 AA; 98931 MW; C7D24EE10136FEDC	CRC64;			

Query Match 54.7%; Score 76; DB 1; Length 860;
Best Local Similarity 46.2%; Pred. No. 0.00088;
Matches 12; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY	1	RILAVERYLKDQQLGIWGCGKLC	26
Db	577	RVTAIEKYLKHQAQLNSWGCAFRQC	602

Search completed: May 3, 2004, 06:25:32
Job time : 25 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 3, 2004, 06:21:53 ; Search time 37 Seconds
(without alignments)
67.594 Million cell updates/sec

Title: US-09-733-239-1
Perfect score: 139
Sequence: 1 RILAVERYLKDQQLGIWGCSGKLIIC 26

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 72

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 50%
Maximum Match 100%
Listing first 500 summaries

Database : PIR 78:*
1: piri:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	139	100.0	357	S21996	envelope protein g
2	139	100.0	358	S21998	envelope protein g
3	139	100.0	853	S54384	envelope polyprote
4	139	100.0	854	S13288	env protein - huma
5	139	100.0	855	VCLJZR	env polyprotein pr
6	139	100.0	856	VCLJH3	env polyprotein pr
7	139	100.0	856	VCLJVL	env polyprotein pr
8	139	100.0	861	VCLJLV	env polyprotein pr
9	138	99.3	357	S22006	envelope protein g
10	138	99.3	357	S21994	envelope protein g
11	138	99.3	357	S22004	envelope protein g
12	138	99.3	357	S21992	envelope protein g
13	138	99.3	856	VCLJBR	env polyprotein -
14	137	98.6	856	A44963	env polyprotein pr
15	135	97.1	357	S21990	envelope protein g
16	135	97.1	358	S22002	envelope protein g
17	135	97.1	358	S22000	envelope protein g
18	135	97.1	358	S70417	envelope protein g
19	135	97.1	443	C41621	env polyprotein p
20	135	97.1	445	A41621	env polyprotein M
21	135	97.1	454	A41621	env polyprotein D
22	135	97.1	843	H44001	env polyprotein pr
23	135	97.1	852	T12016	envelope glycoprot
24	135	97.1	855	VCLJA2	env polyprotein pr
25	135	97.1	856	VCLJ3W	env polyprotein pr
26	135	97.1	861	VCLJSC	env polyprotein pr
27	135	97.1	868	VCLJH4	env polyprotein -
28	134	96.4	859	VCLJMN	env polyprotein pr
29	132	95.0	729	VCLJFX	env polyprotein pr

30	132	95.0	851	2	S33985	env polyprotein -
31	132	95.0	861	1	VCLJKB	env polyprotein pr
32	131	94.2	847	2	T09448	envelope glycoprot
33	131	94.2	847	2	S13289	env protein - huma
34	125	89.9	846	1	VCLJND	env polyprotein pr
35	123	88.5	854	1	VCLJSI	env polyprotein pr
36	120	86.3	859	2	T01672	envelope polyprote
37	98	70.5	863	2	A53034	gag polyprotein -
38	92	66.2	877	2	S49197	envelope protein p
39	91	65.5	104	2	S52930	GP41 ENV protein -
40	89	64.0	855	2	A45713	Env transmembrane
41	86	61.9	859	1	VCLJST	env polyprotein pr
42	84	60.4	869	2	A47665	env protein gp120(
43	84	60.4	881	2	S30368	env protein - huma
44	83	59.7	151	2	S30458	env protein - huma
45	83	59.7	151	2	S30459	env protein - huma
46	83	59.7	151	2	S30448	env protein - huma
47	83	59.7	151	2	S30453	env protein - huma
48	83	59.7	151	2	S30452	env protein - huma
49	83	59.7	151	2	S30450	env protein - huma
50	83	59.7	151	2	S30451	env protein - huma
51	83	59.7	151	2	S30457	env protein - huma
52	83	59.7	151	2	S30456	env protein - huma
53	83	59.7	151	2	S30455	env protein - huma
54	83	59.7	151	2	S30454	env protein - huma
55	83	59.7	366	2	B41565	env polyprotein -
56	83	59.7	712	1	VCLJSA	env polyprotein pr
57	83	59.7	732	2	S46352	env polyprotein -
58	83	59.7	851	2	S12159	env protein - huma
59	83	59.7	852	1	VCLJGG	env polyprotein pr
60	83	59.7	859	1	VCLJCT	env polyprotein pr
61	83	59.7	859	2	S24571	env protein - huma
62	83	59.7	869	2	S53098	envelope polyprote
63	83	59.7	881	1	VCLJG3	env polyprotein -
64	83	59.7	885	2	S04322	env protein - simi
65	83	59.7	886	2	T11555	envelope glycoprot
66	83	59.7	887	2	T11566	env polyprotein -
67	82	59.0	877	2	C46356	env polyprotein -
68	81	58.3	864	1	VCLJG4	env polyprotein -
69	81	58.3	880	1	VCLJG2	env polyprotein pr
70	80	57.6	889	1	VCLJG5	env polyprotein -
71	79	56.8	786	2	S28084	env polyprotein -
72	79	56.8	858	1	VCLJG2	env polyprotein pr

ALIGNMENTS

RESULT 1

S21996
envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 27L)
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
C:Accession: S70422; S21996
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cereb
A:Reference number: S70417; MUID:92144209; PMID:1736940
A:Accession: S70422
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-357 <S2>
A:Cross-references: EMBL:X61356; NID:g60181; PIDN:CAA43624.1; PID:g1067129
A:Experimental source: patient 27L
A:Note: submitted to the EMBL Data Library, July 1991
C:Superfamily: type E retrovirus env polyprotein

Query Match 100.0%; Score 139; DB 2; Length 357;
Best Local Similarity 100.0%; Pred. No. 2.1e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLIIC 26

|||||

Db 80 RILAVERYLKDQQLGIWGCSGKLC 105

RESULT 2
S21998
env polyprotein gp120/gp41 - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
A:Variety: isolate 28
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000
C:Accession: S21998; S70425
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
Submitted to the EMBL Data Library, July 1991
A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined by PCR
A:Reference number: S21998
A:Accession: S21998
A:Molecule type: DNA
A:Residues: 1-358 <STE1>
A:Cross-references: EMBL:X61359; NID:g60182; PIDN:CAA43630.1; PID:g60183
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid
A:Reference number: S70417; MUID:92144209; PMID:1736940
A:Accession: S70425
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-222, 'X', 224-358 <STE2>
A:Cross-references: EMBL:X61359; NID:g60182; PIDN:CAA43630.1; PID:g60183
C:Superfamily: type E retrovirus env polyprotein

Query Match 100.0%; Score 139; DB 2; Length 358;
Best Local Similarity 100.0%; Pred. No. 2.1e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLC 26
|||||
Db 81 RILAVERYLKDQQLGIWGCSGKLC 106

RESULT 3
S54384
env polyprotein - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 26-Aug-1999
C:Accession: S54384
R:Theodore, T.; Buckler-White, A.J.
Submitted to the EMBL Data Library, July 1989
A:Reference number: S54377
A:Accession: S54384
A:Status: preliminary
A:Molecule type: genomic RNA
A:Residues: 1-853 <THE>
A:Cross-references: EMBL:M22639; NID:g329377; PIDN:AAA45370.1; PID:g329385
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: polyprotein

Query Match 100.0%; Score 139; DB 2; Length 853;
Best Local Similarity 100.0%; Pred. No. 5.2e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLC 26
|||||
Db 576 RILAVERYLKDQQLGIWGCSGKLC 601

RESULT 4
S13288
env protein - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Oct-1997
C:Accession: S13288
R:O'Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.Q.; Diagne, A.; Idler, K.; Zack, J.A.
Nature 348, 69-73, 1990
A:Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp120

A:Reference number: S13288; MUID:91043044; PMID:2172833
A:Accession: S13288
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-854 <OBR>
C:Superfamily: type E retrovirus env polyprotein

Query Match 100.0%; Score 139; DB 2; Length 854;
Best Local Similarity 100.0%; Pred. No. 5.2e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLC 26
|||||
Db 577 RILAVERYLKDQQLGIWGCSGKLC 602

RESULT 5
VCLJZR
env polyprotein precursor - human immunodeficiency virus Zr-6
N:Alternate names: coat polyprotein
C:Species: human immunodeficiency virus Zr-6
C:Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 16-Jul-1999
C:Accession: D26192
R:Srinivasan, A.; Anand, R.; York, D.; Ranganathan, P.; Feorino, P.; Schochetman, G.; Cu
Gene 52, 71-82, 1987
A:Title: Molecular characterization of human immunodeficiency virus from Zaire: nucleot
A:Reference number: A26192; MUID:87248097; PMID:3036660
A:Accession: D26192
A:Molecule type: DNA
A:Residues: 1-855 <SRI>
A:Cross-references: GB:X03458; GB:M16322; NID:g329398; PIDN:AAA45380.1; PID:g329403
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-855/Product: env polyprotein #status predicted <MAT>
F:20-500/Product: exterior membrane glycoprotein #status predicted <EXT>
F:501-855/Product: transmembrane glycoprotein #status predicted <TM>
F:187,129,140,145,158,186,189,199,236,243,264,278,291,297,333,340,355,386,392,398,404

Query Match 100.0%; Score 139; DB 1; Length 855;
Best Local Similarity 100.0%; Pred. No. 5.3e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCSGKLC 26
|||||
Db 578 RILAVERYLKDQQLGIWGCSGKLC 603

RESULT 6
VCLJH3
env polyprotein precursor - human immunodeficiency virus type 1 (isolate HTLV-III, BH10)
N:Alternate names: coat polyprotein
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C:Accession: A03973
R:Ratner, L.; Haseltine, W.; Patarca, R.; Livak, K.J.; Starcich, B.; Josephs, S.F.; Dora
nberger, J.A.; Papas, T.S.; Grayeb, J.; Chang, N.T.; Gallo, R.C.; Wong-Staal, F.
Nature 313, 277-284, 1985
A:Title: Complete nucleotide sequence of the AIDS virus, HTLV-III.
A:Reference number: A93353; MUID:85111123; PMID:2578615
A:Accession: A03973
A:Molecule type: DNA
A:Residues: 1-856 <RAT>
A:Cross-references: GB:M15654; GB:X02008; GB:X02009; GB:X02010; NID:g326383; PIDN:AAA4442
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-511/Product: exterior membrane glycoprotein #status predicted <EXT>

F:512-856/Product: transmembrane glycoprotein #status predicted <TMM>
F:88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,402,411,416,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 139; DB 1; Length 856;
Best Local Similarity 100.0%; Pred. No. 5.3e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RILAVERYLKDQQLLGIWGCGSKLIC 26
|||||
Db 579 RILAVERYLKDQQLLGIWGCGSKLIC 604
|||||

RESULT 7
VCLJVL
env polyprotein precursor - human immunodeficiency virus type 1 (isolate LV)
N:Alternate names: coat polyprotein
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C:Accession: A03974
R:Muesing, M.A.; Smith, D.H.; Cabradilla, C.D.; Benton, C.V.; Lasky, L.A.; Capon, D.J.
Nature 313, 450-458, 1985
A:Title: Nucleic acid structure and expression of the human AIDS/lymphadenopathy retrovi
A:Reference number: A93355; MUID:85111157; PMID:2982104
A:Accession: A03974
A:Molecule type: DNA
A:Residues: 1-856 <MUE>
A:Cross-references: GB:K02083; NID:g555008; PIDN:AAB59873.1; PID:g328559
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-511/Product: exterior membrane glycoprotein #status predicted <EXT>
F:512-856/Product: transmembrane glycoprotein #status predicted <TMM>
F:88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,402,411,416,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status predic

Query Match 100.0%; Score 139; DB 1; Length 856;
Best Local Similarity 100.0%; Pred. No. 5.3e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RILAVERYLKDQQLLGIWGCGSKLIC 26
|||||
Db 579 RILAVERYLKDQQLLGIWGCGSKLIC 604
|||||

RESULT 8
VCLJVL
env polyprotein precursor - human immunodeficiency virus type 1 (isolate LAV-1a)
N:Alternate names: coat polyprotein
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C:Accession: A03975
R:Wain-Hobson, S.; Sonigo, P.; Danos, O.; Cole, S.; Alizon, M.
Cell 40, 9-17, 1985
A:Title: Nucleotide sequence of the AIDS virus, LAV..
A:Reference number: A90866; MUID:85099333; PMID:2981635
A:Accession: A03975
A:Molecule type: DNA
A:Residues: 1-861 <WAI>
A:Cross-references: GB:K02013; NID:g326417; PIDN:AAB59751.1; PID:g326424
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-516/Product: exterior membrane glycoprotein #status predicted <EXT>
F:517-861/Product: transmembrane glycoprotein #status predicted <TMM>
F:88,136,141,146,161,165,191,202,239,246,267,281,294,300,306,337,344,361,391,397,402,411,416,621,630,642,679,755,821/Binding site: carbohydrate (Asn) (covalent) #status predic

RESULT 11

S22004
envelope protein gp120/gp41 - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
A:Variety: isolate 4B
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000
C:Accession: S22004; S70419
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
submitted to the EMBL Data Library, July 1991
A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined
A:Reference number: S21990
A:Accession: S22004
A:Molecule type: DNA
A:Residues: 1-357 <STE1>
A:Cross-references: EMBL:X61353; NID:g60189; PID:CAA43618.1; PID:g60189
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid
A:Reference number: S70417; MUID:92144209; PMID:1736940
A:Accession: S70419
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-292, X', 294-357 <STE2>
A:Cross-references: EMBL:X61353; NID:g60188
C:Superfamily: type E retrovirus env polypeptide

Query Match 99.3%; Score 138; DB 2; Length 357;
Best Local Similarity 96.2%; Pred. No. 3e-13; Mismatches 0; Indels 0; Gaps 0;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSKLIC 26
|:|||||
DB 80 RVLAVERYLKDQQLGIWCGSKLIC 105

RESULT 12

S21992
envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 22)
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
C:Accession: S70424; S21992
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid
A:Reference number: S70417; MUID:92144209; PMID:1736940
A:Accession: S70424
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-357 <ST2>
A:Cross-references: EMBL:X61358; NID:g60177; PID:CAA43628.1; PID:g60178
A:Experimental source: patient 22
A>Note: submitted to the EMBL Data Library, July 1991
C:Superfamily: type E retrovirus env polypeptide

Query Match 99.3%; Score 138; DB 2; Length 357;
Best Local Similarity 96.2%; Pred. No. 3e-13; Mismatches 0; Indels 0; Gaps 0;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSKLIC 26
|:|||||
DB 80 RVLAVERYLKDQQLGIWCGSKLIC 105

RESULT 13

VCLJBR
env polypeptide - human immunodeficiency virus type 1 (isolate BR)
N:Alternate names: coat polypeptide
C:Accession: S22004; S70419
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
submitted to the EMBL Data Library, July 1991
A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined
A:Reference number: S21990
A:Accession: S22004
A:Molecule type: DNA
A:Residues: 1-357 <STE1>
A:Cross-references: EMBL:X61357; NID:g60175; PID:CAA43626.1; PID:g60176
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992

Virology 168, 79-89, 1989

A:Title: Biological and molecular characterization of human immunodeficiency virus (HIV-1)
A:Reference number: A94389; MUID:89085613; PMID:2789516
A:Accession: A31667
A:Molecule type: DNA
A:Residues: 1-852 <ANA>
C:Superfamily: type E retrovirus env polypeptide
C:Keywords: capsid protein; coat protein; polypeptide; transmembrane protein
F:1-516/Product: coat protein gp120 #status predicted <CP1>
F:517-852/Product: coat protein gp41 #status predicted <CP2>

Query Match 99.3%; Score 138; DB 1; Length 852;
Best Local Similarity 96.2%; Pred. No. 7.4e-13; Mismatches 0; Indels 0; Gaps 0;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSKLIC 26
|:|||||
DB 575 RVLAVERYLKDQQLGIWCGSKLIC 600

RESULT 14

A44963
env polypeptide precursor - human immunodeficiency virus type 1 (isolate Z321)
N:Alternate names: coat polypeptide
C:Accession: A44963
C:Keywords: capsid protein; coat protein gp120; coat protein gp41
C:Species: human immunodeficiency virus type 1, HIV-1
A>Note: host Homo sapiens (man)
C:Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 28-May-1999
C:Accession: A44963
R:Srinivasan, A.; York, D.; Butler Jr., D.; Jannoun-Nasr, R.; Getchell, J.; McCormick, J.
AIDS Res. Hum. Retroviruses 5, 121-129, 1989
A:Title: Molecular characterization of HIV-1 isolated from a serum collected in 1976: nu
A:Reference number: A44963; MUID:89228766; PMID:2713163
A:Accession: A44963
A:Molecule type: DNA
A:Residues: 1-856 <SRI>
A:Cross-references: GB:M15896; NID:g329392; PIDN:AAB53948.1; PID:g329394
C:Genetics: env
C:Superfamily: type E retrovirus env polypeptide
C:Keywords: capsid protein; coat protein; glycoprotein; polypeptide; transmembrane prote
F:1-529/Domain: signal sequence #status predicted <SIG>
F:521-856/Product: coat protein gp120 #status predicted <CP1>
F:521-856/Product: coat protein gp41 #status predicted <CP2>
F:684-705/Domain: transmembrane #status predicted <TMN>
F:87,132,138,152,156,183,198,242,263,277,294,302,339,398,402,411,448,461,462,465,611

Query Match 98.6%; Score 137; DB 1; Length 856;
Best Local Similarity 96.2%; Pred. No. 1.1e-12; Mismatches 0; Indels 0; Gaps 0;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWCGSKLIC 26
|:|||||
DB 579 RILAVERYLKDQQLGIWCGSKLIC 604

RESULT 15

S21990
envelope protein gp120/gp41 - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
A:Variety: isolate 20
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000
C:Accession: S21990; S70423
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
submitted to the EMBL Data Library, July 1991
A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined
A:Reference number: S21990
A:Accession: S21990
A:Molecule type: DNA
A:Residues: 1-357 <STE1>
A:Cross-references: EMBL:X61357; NID:g60175; PIDN:CAA43626.1; PID:g60176
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992

Qy 1 RLIAVERYLKDQQLGIWGCGSKLIC 26
:|||||:|||||:|||||
Db 81 RVLAVERYLKDQQLGIWGCGSKLIC 106

RESULT 18
S70417
envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 3B) (fragment)
C:Species: human immunodeficiency virus type 1, HIV-1
A:Variety: patient 3B
C:Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 26-Aug-1999
C:Accession: S70417
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid from patients with AIDS
A:Reference number: S70417; MUID:92144209; PMID:1736940
A:Accession: S70417
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-358 <STE>
A:Cross-references: EMBL:X61351; NID:G60184; PIDN:CAA43614.1; PID:G60185
C:Superfamily: type E retrovirus env polyprotein

Query Match 97.1%; Score 135; DB 2; Length 358;
Best Local Similarity 92.3%; Pred. No. 8.7e-13;
Matches 24; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLIAVERYLKDQQLGIWGCGSKLIC 26
:|||||:|||||:|||||
Db 81 RVLAVERYLKDQQLGIWGCGSKLIC 106

RESULT 19
C41621
env polyprotein P - human immunodeficiency virus type 1 (fragment)
N:Alternate names: coat polyprotein
N:Contents: amino end of coat protein gp41; carboxyl end of coat protein gp120
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 11-Feb-1993 #sequence_revision 31-Dec-1993 #text_change 26-Aug-1999
C:Accession: C41621
R:Burger, H.; Weiser, B.; Flaherty, K.; Gulla, J.; Nguyen, P.N.; Gibbs, R.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991
A:Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity
A:Reference number: A41621; MUID:92107924; PMID:1763038
A:Accession: C41621
A:Molecule type: DNA
A:Residues: 1-443 <BUR>
A:Cross-references: GB:M77230; NID:G328631; PIDN:AAB03792.1; PID:G555015
A:Note: this virus was isolated from the mother's sexual partner
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polypro.
F:1-251/Product: coat protein gp120 (fragment) #status predicted <GP1>
F:252-443/Product: coat protein gp41 (fragment) #status predicted <GP2>
F:424-443/Domain: transmembrane #status predicted <TMN>
F:9,23,36,48,78,101,107,131,137,143,147,153,188,200,203,351,356,365,377/Binding site: c

Query Match 97.1%; Score 135; DB 2; Length 443;
Best Local Similarity 92.3%; Pred. No. 1.1e-12;
Matches 24; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLIAVERYLKDQQLGIWGCGSKLIC 26
:|||||:|||||:|||||
Db 319 RVLAVERYLKDQQLGIWGCGSKLIC 344

RESULT 20
A41621
env polyprotein M - human immunodeficiency virus type 1 (fragment)
N:Alternate names: coat polyprotein


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Best Local Similarity 92.3%; Pred. No. 3.1e-12;
Matches 24; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCCKLIC 26
   |:|||||:|||||:|||||:|||||:
Db 583 RVLAVERYLKDQQLGIWGCCKLIC 608

RESULT 29
VCLJXK
env polyprotein precursor - human immunodeficiency virus type 1 (strain KB-1-gp32)
N:Alternate names: coat polyprotein
N:Contains: coat protein gp120; coat protein gp32
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 01-Mar-1996
C:Accession: B42995
R:Shimizu, H.; Hasebe, F.; Tsuchie, H.; Morikawa, S.; Ushijima, H.; Kitamura, T.
Virology 189, 534-546, 1992
A:Title: Analysis of a human immunodeficiency virus type 1 isolate carrying a truncated
A:Reference number: A42995; MUID:92351552; PMID:1322587
A:Accession: B42995
A:Molecule type: mRNA
A:Residues: 1-729 <SHI>
A:Cross-references: GB:S41266; GB:D01206
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein
F:1-689/Domain: extracellular #status predicted <EXT>
F:1-33/Domain: signal sequence #status predicted <SIG>
F:17-33/Region: hydrophobic #status predicted
F:34-517/Product: coat protein gp120 #status predicted <CP1>
F:514-517/Region: cleavage processing #status predicted <CP2>
F:518-729/Product: coat protein gp32 #status predicted <CP2>
F:518-534/Region: hydrophobic #status predicted
F:690-711/Domain: transmembrane #status predicted <TM1>
F:712-729/Domain: intracellular #status predicted <INT>
F:93.141,145,146,163,191,192,237,241,248,269,283,296,308,338,345,361,367,397,403,408,414

Query Match 95.0%; Score 132; DB 1; Length 729;
Best Local Similarity 88.5%; Pred. No. 5.2e-12;
Matches 23; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCCKLIC 26
   |:|||||:|||||:|||||:|||||:
Db 585 RVLAVERYLKDQQLGIWGCCKLIC 610

RESULT 30
S33985
env polyprotein - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 26-Aug-1999
C:Accession: S33985
R:Carlini, F.
submitted to the EMBL Data Library, November 1991
A:Reference number: S33979
A:Accession: S33985
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-851 <CAR>
A:Cross-references: EMBL:Z11530; NID:g60192; PIDN:CAA77628.1; PID:g60199
C:Superfamily: type E retrovirus env polyprotein

Query Match 95.0%; Score 132; DB 2; Length 851;
Best Local Similarity 96.2%; Pred. No. 6.2e-12;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCCKLIC 26
   |:|||||:|||||:|||||:|||||:
Db 574 RILAVERYLKDQQLGIWGCCKLIC 599
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RESULT 31
VCLJKB
env polyprotein precursor - human immunodeficiency virus type 1 (strain KB-1-gp41)
N:Alternate names: coat polyprotein
N:Contains: coat protein gp120; coat protein gp41
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 01-Mar-1996
C:Accession: A42995
R:Shimizu, H.; Hasebe, F.; Tsuchie, H.; Morikawa, S.; Ushijima, H.; Kitamura, T.
Virology 189, 534-546, 1992
A:Title: Analysis of a human immunodeficiency virus type 1 isolate carrying a truncated
A:Reference number: A42995; MUID:92351552; PMID:1322587
A:Accession: A42995
A:Molecule type: mRNA
A:Residues: 1-861 <SHI>
A:Cross-references: GB:S41266; GB:D01206
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein
F:1-689/Domain: extracellular #status predicted <EXT>
F:1-33/Domain: signal sequence #status predicted <SIG>
F:17-33/Region: hydrophobic #status predicted
F:34-517/Product: coat protein gp120 #status predicted <CP1>
F:514-517/Region: cleavage processing #status predicted <CP2>
F:518-861/Product: coat protein gp41 #status predicted <CP2>
F:518-534/Region: hydrophobic #status predicted
F:690-711/Domain: transmembrane #status predicted <TM1>
F:712-861/Domain: intracellular #status predicted <INT>
F:756-772/Region: hydrophobic #status predicted
F:93.141,145,146,163,191,192,237,241,248,269,283,296,308,338,345,361,367,397,403,408,414

Query Match 95.0%; Score 132; DB 1; Length 861;
Best Local Similarity 88.5%; Pred. No. 6.2e-12;
Matches 23; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCCKLIC 26
   |:|||||:|||||:|||||:|||||:
Db 585 RVLAVERYLKDQQLGIWGCCKLIC 610

RESULT 32
T09448
envelope glycoprotein - human immunodeficiency virus type 1 (strain JRFL)
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 24-Nov-1999
C:Accession: T09448
R:Pang, S.; Vinters, H.V.; Akashi, T.; O'Brien, W.A.; Chen, I.S.; Koyanagi, Y.; Namazie,
submitted to the EMBL Data Library, July 1996
A:Reference number: Z16673
A:Accession: T09448
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-847 <PAN>
A:Cross-references: EMBL:U63632; NID:g1465777; PID:g1465781
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein

Query Match 94.2%; Score 131; DB 2; Length 847;
Best Local Similarity 92.3%; Pred. No. 8.7e-12;
Matches 24; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIWGCCKLIC 26
   |:|||||:|||||:|||||:|||||:
Db 570 RVLAVERYLKDQQLGIWGCCKLIC 595

RESULT 33
S13289
env protein - human immunodeficiency virus type 1
```

C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Oct-1997
C:Accession: S13289
R:O'Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.Q.; Diagne, A.; Idler, K.; Zack, J.A.
Nature 348, 69-73, 1990
A:Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp120
A:Reference number: S13288; MUID:91043044; PMID:2172833
A:Accession: S13289
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-847 <OBR>
C:Superfamily: type E retrovirus env polypeptide

Query Match 94.2%; Score 131; DB 2; Length 847;
Best Local Similarity 92.3%; Pred. No. 8.7e-12;
Matches 24; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 R1LAVERYLKDQQLGIWCGSGKLC 26
DB 570 RVLAVERYLQDQQLGIWCGSGKLC 595
|:|||||:|||||:|||||:|||||:|

RESULT 34
VCLJND
env polypeptide precursor - human immunodeficiency virus type 1 (isolate NDK)
N;Alternate names: coat polypeptide
N;Contains: coat protein gp120; coat protein gp41
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999
C:Accession: JQ0066
R:Spire, B.; Sire, J.; Zachar, V.; Rey, F.; Barre-Sinoussi, F.; Galibert, F.; Hampe, A.;
Gene 81, 275-284, 1989
A:Title: Nucleotide sequence of HIV-1-NDK: a highly cytopathic strain of the human immunodeficiency virus
A:Reference number: JQ0065; MUID:90034200; PMID:2806917
A:Accession: JQ0066
A:Molecule type: DNA
A:Residues: 1-846 <SPI>
A:Cross-references: GB:M27323; NID:G328154; PIDN:AAA44873.1; PID:G328162
A:Note: the authors translated the codon GCG for residue 523 as Arg
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polypeptide
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polypeptide
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-501/Product: coat protein gp120 #status predicted <CP1>
F:502-846/Product: coat protein gp41 #status predicted <CP2>
F:502-520/Domain: transmembrane #status predicted <TM1>
F:574-692/Domain: transmembrane #status predicted <TM2>
F:87,129,151,179,182,229,236,257,271,284,290,351,382,388,392,395,401,438,451,452,601,606

Query Match 89.9%; Score 125; DB 1; Length 846;
Best Local Similarity 84.8%; Pred. No. 7.2e-11;
Matches 22; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 R1LAVERYLKDQQLGIWCGSGKLC 26
DB 569 RVLAVERYLQDQQLGIWCGSGKLC 594
|:|||||:|||||:|||||:|||||:|

RESULT 35
VCLJSI
env polypeptide precursor - simian immunodeficiency virus SIVcpz
N;Alternate names: coat polypeptide
N;Contains: coat protein gp120; coat protein gp41
C:Species: simian immunodeficiency virus SIVcpz
A:Note: host Pan troglodytes (chimpanzee)
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999
C:Accession: S09990
R:Ruet, T.; Chevnyier, R.; Meyerhans, A.; Roelants, G.; Wain-Hobson, S.
Nature 345, 356-359, 1990
A:Title: Genetic organization of a chimpanzee lentivirus related to HIV-1.
A:Reference number: S09983; MUID:90259077; PMID:2188136

C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Oct-1997
C:Accession: S13289
R:O'Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.Q.; Diagne, A.; Idler, K.; Zack, J.A.
Nature 348, 69-73, 1990
A:Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp120
A:Reference number: S13288; MUID:91043044; PMID:2172833
A:Accession: S13289
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-854 <HUB>
C:Cross-references: EMBL:X52154; NID:g58866; PIDN:CAA36407.1; PID:g58874
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polypeptide
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polypeptide
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-500/Product: coat protein gp120 #status predicted <CP1>
F:501-854/Product: coat protein gp41 #status predicted <CP2>
F:501-517/Domain: transmembrane #status predicted <TM1>
F:675-693/Domain: transmembrane #status predicted <TM2>
F:805-821/Domain: transmembrane #status predicted <TM3>
F:134,140,143,154,158,186,195,239,260,267,274,299,331,336,351,356,384,392,426,432,446,4

Query Match 88.5%; Score 123; DB 1; Length 854;
Best Local Similarity 76.9%; Pred. No. 1.5e-10;
Matches 20; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 R1LAVERYLKDQQLGIWCGSGKLC 26
DB 569 RVLAVERYLQDQQLGIWCGSGKLC 594
|:|||||:|||||:|||||:|||||:|

RESULT 36
T01672
env polypeptide precursor - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 21-Jul-2000
C:Accession: T01672
R:Alizon, M.; Wain-Hobson, S.; Gluckman, J.C.; Sonigo, P.
Cell 46, 63-74, 1996
A:Title: Genetic variability of the AIDS virus: Nucleotide sequence analysis of two iso
A:Reference number: Z14389; MUID:86245056; PMID:2424612
A:Accession: T01672
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-859 <ALI>
A:Cross-references: EMBL:K03456; NID:g60228; PIDN:CAA28016.1; PID:g60234
C:Superfamily: type E retrovirus env polypeptide

Query Match 86.3%; Score 120; DB 2; Length 859;
Best Local Similarity 80.8%; Pred. No. 4.3e-10;
Matches 21; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 R1LAVERYLKDQQLGIWCGSGKLC 26
DB 581 RVLAVERYLQDQQLGIWCGSGKLC 606
|:|||||:|||||:|||||:|||||:|

RESULT 37
AS3034
gag polypeptide - human immunodeficiency virus type 1 (strain Ant70)
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 07-May-1999
C:Accession: AS3034
R:Vanden Haesevelde, M.; Decourt, J.L.; De Leys, R.J.; Vanderborgh, B.; van der Groen,
J. Virol. 68, 1586-1596, 1994
A:Title: Genomic cloning and complete sequence analysis of a highly divergent African h
A:Reference number: AS3034; MUID:94149849; PMID:8107220
A:Accession: AS3034
A>Status: preliminary
A:Molecule type: genomic RNA
A:Residues: 1-863 <VAN>
A:Cross-references: GB:L02587
C:Superfamily: type E retrovirus env polypeptide
C:Keywords: polypeptide

Query Match 70.5%; Score 98; DB 2; Length 863;
Best Local Similarity 61.5%; Pred. No. 1e-06;
Matches 16; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

```

Qy      1 RILAVERYLKDQQLGIWGCCKLIC 26
          |::|||::|||::|||::|||
Db      581 RLALLETLLNQQLSLWGCKGKLV 606

RESULT 38
S49197
envelope protein precursor - human immunodeficiency virus type 1 (fragment)
C:Species: human immunodeficiency virus type 1, HIV-1
C>Date: 19-Mar-1997 #sequence_revision 24-Jul-1997 #text_change 26-Aug-1999
C:Accession: S49197
F:Charneau, P.; Borman, A.M.; Quillent, C.; Guetard, D.; Chamaret, S.; Cohen, J.; Remy,
A:Description: Isolation and envelope sequence of a highly divergent HIV-1 isolate: defi
A:Reference number: S49197
A:Accession: S49197
A:Molecule type: DNA
A:Residues: 1-877 <CHA>
A:Cross-references: EMBL:X80020; NID:g510516; PIDN:CAA56323.1; PID:g510517
A:Experimental source: Isolate VAU
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: Glycoprotein; capsid protein; coat protein; transmembrane protein
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-535/Product: coat protein gp120 #status predicted <CP1>
F:536-877/Product: coat protein gp41 #status predicted <CP2>
F:698-716/Domain: transmembrane #status predicted <TMN>
F:59, 88, 139, 148, 159, 184, 188, 198, 230, 235, 242, 263, 270, 277, 292, 302, 333, 345, 357, 367, 396, 404,

Query Match      66.2%; Score 92; DB 2; Length 877;
Best Local Similarity 53.8%; Pred. No. 8.4e-06;
Matches 14; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

Qy      1 RILAVERYLKDQQLGIWGCCKLIC 26
          |::|||::|||::|||::|||
Db      594 RLALETFIONQQLNLWGCKNRLLIC 619

RESULT 39
S52930
GP41 ENV protein - human immunodeficiency virus type 1 (fragment)
C:Species: human immunodeficiency virus type 1, HIV-1
C>Date: 06-Jun-1995 #sequence_revision 21-Jul-1995 #text_change 26-Aug-1999
C:Accession: S52930
R:Cohen, J.H.M.; Guetard, D.; Philibert, F.; Chamaret, S.; Tabary, T.; Montagnier, L.; de
submitted to the EMBL Data Library, January 1995
A:Description: A novel HIV1-O strain illustrates the diversity of the O group.
A:Reference number: S52929
A:Accession: S52930
A>Status: preliminary
A:Molecule type: genomic RNA
A:Residues: 1-104 <COH>
A:Cross-references: EMBL:X84328; NID:g695526; PIDN:CAA59066.1; PID:g695527
C:Superfamily: type E retrovirus env polyprotein

Query Match      65.5%; Score 91; DB 2; Length 104;
Best Local Similarity 57.7%; Pred. No. 1.3e-06;
Matches 15; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy      1 RILAVERYLKDQQLGIWGCCKLIC 26
          |::|||::|||::|||::|||
Db      32 RLALLETLMQNQQLNLWGCRGAIC 57

RESULT 40
A45713
Env transmembrane protein gp43 - human immunodeficiency virus type 2
C:Species: human immunodeficiency virus type 2, HIV-2
C>Date: 04-Mar-1994 #sequence_revision 18-Nov-1994 #text_change 12-Apr-1995
C:Accession: A45713
F:Barnett, S.W.; Quiroga, M.; Werner, A.; Dina, D.; Levy, J.A.
J. Virol. 67, 1006-1014, 1993
A:title: Distinguishing features of an infectious molecular clone of the highly divergen

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Query Match 60.4%; Score 84; DB 2; Length 869;
Best Local Similarity 50.0%; Pred. No. 0.00014;
Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIGWCSGKLC 26
DB 592 RVTAEIKYLDQAQLNSWGCAFRQVC 617

RESULT 43

S30368

env protein - human T-cell lymphotropic virus type 4

C:Species: human T-cell lymphotropic virus type 4, HTLV-4

C:Date: 21-Nov-1993 #sequence_revision 26-May-1995 #text_change 03-May-1996

C:Accession: S03068

R:Hahn, B.H.; Kong, L.I.; Lee, S.W.; Kumar, P.; Taylor, M.E.; Arya, S.K.; Shaw, G.M.

Nature 300, 184-186, 1987

A:Title: Relation of HTLV-4 to simian and human immunodeficiency-associated viruses.

A:Reference number: S03065

A:Accession: S03068

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-881 <HAH>

A:Cross-references: EMBL:X06391

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1987
C:Superfamily: type E retrovirus env polypeptide

Query Match 60.4%; Score 84; DB 2; Length 881;
Best Local Similarity 50.0%; Pred. No. 0.00014;
Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIGWCSGKLC 26
DB 594 RVTAEIKYLDQAQLNSWGCAFRQVC 619

RESULT 44

S30458

env protein - human immunodeficiency virus type 2 (fragment)

C:Species: human immunodeficiency virus type 2, HIV-2

C:Date: 02-Dec-1993 #sequence_revision 30-Jan-1998 #text_change 23-Mar-2001

C:Accession: S30458; S30477

R:Gao, F.; Yue, L.; White, A.T.; Pappas, P.G.; Barchue, J.; Hanson, A.P.; Greene, B.M.;

Nature 358, 495-499, 1992

A:Title: Human infection by genetically diverse SIV(SM)-related HIV-2 in West Africa.

A:Reference number: S30448; MUID:92350299; PMID:1641038

A:Accession: S30458

A:Molecule type: nucleic acid

A:Residues: 1-151 <GAO>

A:Cross-references: EMBL:M87142

R:Gao, F.; Yue, L.; White, A.T.; Pappas, P.G.; Barchue, J.; Hanson, A.P.; Greene, B.M.;

submitted to the EMBL Data Library, December 1992

A:Description: Human infection by genetically diverse SIVSM-related HIV-2 in west Africa

A:Reference number: S30460

A:Accession: S30477

A:Status: preliminary

A:Molecule type: nucleic acid

A:Residues: 1-151 <GA2>

A:Cross-references: EMBL:M87141

C:Genetics:

C:Gene: env

C:Superfamily: type E retrovirus env polypeptide

C:Keywords: coat protein; glycoprotein

Query Match 59.7%; Score 83; DB 2; Length 151;
Best Local Similarity 50.0%; Pred. No. 3.2e-05;
Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIGWCSGKLC 26
DB 23 RVTAEIKYLDQAQLNSWGCAFRQVC 48

RESULT 45

S30459

env protein - human immunodeficiency virus type 2 (fragment)

C:Species: human immunodeficiency virus type 2, HIV-2

C:Date: 02-Dec-1993 #sequence_revision 30-Jan-1998 #text_change 17-Mar-1999

C:Accession: S30459

R:Gao, F.; Yue, L.; White, A.T.; Pappas, P.G.; Barchue, J.; Hanson, A.P.; Greene, B.M.;

Nature 358, 495-499, 1992

A:Title: Human infection by genetically diverse SIV(SM)-related HIV-2 in West Africa.

A:Reference number: S30448; MUID:92350299; PMID:1641038

A:Accession: S30459

A:Status: translation not shown

A:Molecule type: nucleic acid

A:Residues: 1-151 <GAO>

A:Cross-references: EMBL:M87143

C:Genetics:

C:Gene: env

C:Superfamily: type E retrovirus env polypeptide

C:Keywords: coat protein; glycoprotein

Query Match 59.7%; Score 83; DB 2; Length 151;
Best Local Similarity 50.0%; Pred. No. 3.2e-05;
Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQQLGIGWCSGKLC 26
DB 23 RVTAEIKYLDQAQLNSWGCAFRQVC 48

RESULT 46

S30448

env protein - human immunodeficiency virus type 2 (fragment)

C:Species: human immunodeficiency virus type 2, HIV-2

C:Date: 02-Dec-1993 #sequence_revision 30-Jan-1998 #text_change 17-Mar-1999

C:Accession: S30448; S30449; S30480; S30481

R:Gao, F.; Yue, L.; White, A.T.; Pappas, P.G.;

Nature 358, 495-499, 1992

A:Title: Human infection by genetically diverse SIV(SM)-related HIV-2 in West Africa.

A:Reference number: S30448; MUID:92350299; PMID:1641038

A:Accession: S30448

A:Molecule type: nucleic acid

A:Residues: 1-151 <GAO>

A:Cross-references: EMBL:M87069

A:Experimental source: FOENVA13

A:Accession: S30449

A:Status: preliminary; translation not shown

A:Molecule type: nucleic acid

A:Residues: 1-151 <GAW>

A:Cross-references: EMBL:M87071

A:Experimental source: FOENVA3

R:Gao, F.; Yue, L.; White, A.T.; Pappas, P.G.; Barchue, J.; Hanson, A.P.; Greene, B.M.;

submitted to the EMBL Data Library, December 1992

A:Description: Human infection by genetically diverse SIVSM-related HIV-2 in west Africa

A:Reference number: S30460

A:Accession: S30480

A:Status: preliminary

A:Molecule type: nucleic acid

A:Residues: 1-151 <GA2>

A:Cross-references: EMBL:M87085

A:Accession: S30481

A:Status: preliminary

A:Molecule type: nucleic acid

A:Residues: 1-151 <GA3>

A:Cross-references: EMBL:M87076

C:Genetics:

C:Gene: env

C:Superfamily: type E retrovirus env polypeptide

C:Keywords: coat protein; glycoprotein

Query Match 59.7%; Score 83; DB 2; Length 151;
Best Local Similarity 50.0%; Pred. No. 3.2e-05;
Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 RILAVERYLKDQLLGIWCSGKLIC 26
| : | : | : | : | : | : | : | : | : |
Db 23 RVTAIEKYLKDOAKLSWGCAFRVC 48

RESULT 52

env protein - human immunodeficiency virus type 2 (fragment)
 C;Species: human immunodeficiency virus type 2, HIV-2
 C;Date: 02-Dec-1993 #sequence_revision 30-Jan-1998 #text_change 17-Mar-1999
 C;Accession: S30456
 R;Gao, F.; Yue, L.; White, A.T.; Pappas, P.G.; Barchue, J.; Hanson, A.P.; Greene, B.M.;
 Nature 358, 495-499, 1992
 A;Title: Human infection by genetically diverse SIV(SM)-related HIV-2 in West Africa.
 A;Reference number: S30448; MUID:92350299; PMID:1641038
 A;Accession: S30456
 A;Status: translation not shown
 A;Molecule type: nucleic acid
 A;Residues: 1-151 <GAO>
 A;Cross-references: EMBL:M87129
 C;Genetics: env
 A;Gene: env
 C;Superfamily: type E retrovirus env polyprotein
 C;Keywords: coat protein; glycoprotein

Query Match 59.7%; Score 83; DB 2; Length 151;
Best Local Similarity 50.0%; Pred. No. 3.2e-05;
Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy 1 RILAVERYLKDQQLGIWCSGKLIC 26
 | : | : | : | : | : | : |
Db 23 RVTAIEKYLKDOAKLNSWGCAFRVC 48

RESULT 53

S30455
env protein - human immunodeficiency virus type 2 (fragment)
C:Species: human immunodeficiency virus type 2, HIV-2
C:Date: 02-Dec-1993 #sequence revision 30-Jan-1998 #text_change 23-Mar-2001
C:Accession: S30455; S30461; S30469
R:Gao, F.; Yue, L.; White, A.T.; Pappas, P.G.; Barchue, J.; Greene, B.M.;
Nature 358, 495-499, 1992
A:Title: Human infection by genetically diverse SIV(SM)-related HIV-2 in West Africa.
A:Reference number: S30448; PMID:92350299; PMID:1641038
A:Accession: S30455
A:Status: translation not shown
A:Molecule type: nucleic acid
A:Residues: 1-151 <GA0>
A:Cross-references: EMBL:M87123
R:Gao, F.; Yue, L.; White, A.T.; Pappas, P.G.; Barchue, J.; Hanson, A.P.; Greene, B.M.;
submitted to the EMBL Data Library, December 1992
A:Description: Human infection by genetically diverse SIVSM-related HIV-2 in west Africa
A:Reference number: S30460
A:Accession: S30461
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-151 <GA2>
A:Cross-references: EMBL:M87131
A:Accession: S30469
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-151 <GA3>
A:Cross-references: EMBL:M87122
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: coat protein; glycoprotein

Query Match 59.7%; Score 83; DB 2; Length 151;
Best Local Similarity 50.0%; Pred. No. 3.2e-05;
Matches 13; Conservative 6; Mismatches 7; Indels

1 R1LAVERYLKDQQLLGIWGCSGKLC 26 QY

23 RVTAEIKYLKDOAKLNSWGCAFCVOC 48

RESULT 54

env protein - human immunodeficiency virus type 2 (fragment)
C/Species: human immunodeficiency virus type 2, HIV-2
C/Date: 09-May-1997 #sequence revision 09-May-1997 #text change 17-Mar-1999
C/Accession: S30465; S30460; S30462; S30463; S30464; S30466; S30467; S30468; S30470; S30471
R/Gao, F.; Yue, L.; White, A.T.; Pappas, P.G.; Barchue, J.; Hanson, A.P.; Greene, B.M.;
submitted to the EMBL Data Library, December 1992
A/Description: Human infection by genetically diverse SIVSM-related HIV-2 in west Africa
A/Reference number: S30460
A/Accession: S30465
A/Status: preliminary
A/Molecule type: nucleic acid
A/Residues: 1-151 <GAO>
A/Cross-references: EMBL:M87128
A/Accession: S30460
A/Molecule type: nucleic acid
A/Residues: 1-151 <GAW>
A/Cross-references: EMBL:M87120
A/Experimental source: clone 22ENVB15
A/Accession: S30462
A/Molecule type: nucleic acid
A/Residues: 1-151 <GAF>
A/Cross-references: EMBL:M87132
A/Experimental source: clone 22ENVB4
A/Accession: S30463
A/Molecule type: nucleic acid
A/Residues: 1-151 <GAA>
A/Cross-references: EMBL:M87126
A/Experimental source: clone 22ENVBB3
A/Accession: S30464
A/Molecule type: nucleic acid
A/Residues: 1-151 <GAZ>
A/Cross-references: EMBL:M87127
A/Experimental source: clone 22ENVBB4
A/Accession: S30466
A/Molecule type: nucleic acid
A/Residues: 1-151 <GAY>
A/Cross-references: EMBL:M87121
A/Experimental source: clone 22ENVB17
A/Accession: S30467
A/Molecule type: nucleic acid
A/Residues: 1-151 <GAH>
A/Cross-references: EMBL:M87119
A/Experimental source: clone 22ENVB11
A/Accession: S30468
A/Molecule type: nucleic acid
A/Residues: 1-151 <GAS>
A/Cross-references: EMBL:M87133
A/Experimental source: clone 22ENVB5
A/Accession: S30470
A/Molecule type: nucleic acid
A/Residues: 1-151 <GAN>
A/Cross-references: EMBL:M87134
A/Experimental source: clone 22ENVB8
A/Accession: S30471
A/Molecule type: nucleic acid
A/Residues: 1-151 <GAG>
A/Cross-references: EMBL:M87124
A/Experimental source: clone 22ENVBB1
A/Accession: S30472
A/Molecule type: nucleic acid
A/Residues: 1-151 <GAC>
A/Cross-references: EMBL:M87125
A/Experimental source: clone 22ENVBB2
R/Gao, F.; Yue, L.; White, A.T.; Pappas, P.G.; Barchue, J.; Hanson, A.P.; Greene, B.M.;
Nature 358, 495-499, 1992
A/Title: Human infection by genetically diverse SIV(SM)-related HIV-2 in West Africa.
A/Reference number: S30448; MUID:92350299; PMID:1641038

C:Superfamily: type E retrovirus env polyprotein
 C:Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein
 F.1-19/Domain: signal sequence #status predicted <SIG>

F;1-19/Domain: signal s

[illegible]

```
Db      568 RVTAEIKYLDQQLNSWGCAFRQVC 593

RESULT 59
VCLJGG
env polypeptide precursor - human immunodeficiency virus type 2 (isolate GH-1)
N;Alternate names: coat polypeptide
C:Species: human immunodeficiency virus type 2, HIV-2
A:Note: Host Homo sapiens (man)
C:Date: 30-Jun-1990 #sequence_revision 26-Jan-1996 #text_change 16-Feb-1997
C:Accession: JS0334
R:Hasegawa, A.; Tsujimoto, H.; Maki, N.; Ishikawa, K.; Miura, T.; Fukasawa, M.; Miki, K.
AIDS Res. Hum. Retroviruses 5, 593-604, 1989
A:Title: Sequence of a distinct HIV-2 isolate from Ghana showing significant divergence
A:Reference number: JS0327; MUID:90122350; PMID:2611042
A:Accession: JS0334
A:Molecule type: DNA
A:Residues: 1-852 <HAS>
A:Note: this sequence was submitted to JIPID, October 1989
A:Note: readthrough of the UAG stop codon at 739 may occur
C:Comment: Cleavage sites that yield the mature coat proteins are not determined.
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polypeptide
C:Keywords: AIDS; coat protein; glycoprotein; polypeptide; transmembrane protein
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-852/Product: env polypeptide #status predicted <MAT>
F;36,69,113,117,118,132,141,169,182,197,229,232,263,269,280,291,301,356,362,389,402,439,
Query Match      59.7%; Score 83; DB 1; Length 852;
Best Local Similarity 50.0%; Pred. No. 0.00019;
Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY      1 RILAVERYLKDQQLGWCSGKLC 26
Db      569 RVTAEIKYLDQQLNSWGCAFRQVC 594

RESULT 60
VCLJCT
env polypeptide precursor - human immunodeficiency virus type 2 (isolate CAM2/Guinea-Bissau)
N;Alternate names: coat polypeptide
C:Species: human immunodeficiency virus type 2, HIV-2
A:Note: Host Homo sapiens (man)
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jun-2000
C:Accession: F38475; J00978
R:Tristem, M.; Hill, F.; Karpas, A.
J. Gen. Virol. 72, 721-724, 1991
A:Title: Nucleotide sequence of a Guinea-Bissau-derived human immunodeficiency virus type 2
A:Reference number: A38475; MUID:91170959; PMID:2005437
A:Accession: F38475
A:Molecule type: DNA
A:Residues: 1-859 <TRI>
A:Cross-references: GB:D00835; NID:G3153166; PIDN:BARA00716.1; PID:G221472
C:Comment: The cleavage sites of this polypeptide have not been determined.
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polypeptide
C:Keywords: AIDS; coat protein; glycoprotein; immunodeficiency; polypeptide; transmembrane protein
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-859/Product: env polypeptide #status predicted <ENP>
F;38,71,115,148,163,176,188,195,205,237,247,271,277,288,299,309,343,366,398,411,448,463;
Query Match      59.7%; Score 83; DB 1; Length 859;
Best Local Similarity 50.0%; Pred. No. 0.0002;
Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY      1 RILAVERYLKDQQLGWCSGKLC 26
Db      579 RVTAEIKYLDQQLNSWGCAFRQVC 604

RESULT 61
S24571
env protein - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
C:Accession: S24571
R:Dietrich, U.
submitted to the EMBL Data Library, August 1989
A:Reference number: S24571
A:Accession: S24571
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-859 <DIE>
A:Cross-references: EMBL:X61240; NID:G60256; PIDN:CAA43572.1; PID:G60257
C:Superfamily: type E retrovirus env polypeptide
Query Match      59.7%; Score 83; DB 2; Length 859;
Best Local Similarity 50.0%; Pred. No. 0.0002;
Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY      1 RILAVERYLKDQQLGWCSGKLC 26
Db      580 RVTAEIKYLDQQLNSWGCAFRQVC 605

RESULT 62
S53098
envelope polypeptide - human immunodeficiency virus type 2
C:Species: human immunodeficiency virus type 2, HIV-2
C:Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 26-Aug-1999
C:Accession: S53098
R:Becker, M.; Zorr, B.; Becker, A.; Habermehl, K.O.
submitted to the EMBL Data Library, March 1995
A:Description: Molecular and phylogenetic characterisation of a Guinea-Bissau-derived human immunodeficiency virus type 2
A:Reference number: S53091
A:Accession: S53098
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-869 <BEC>
A:Cross-references: EMBL:Z48731; NID:G732718; PIDN:CAA88627.1; PID:G732736
C:Superfamily: type E retrovirus env polypeptide
C:Keywords: polypeptide
Query Match      59.7%; Score 83; DB 2; Length 869;
Best Local Similarity 50.0%; Pred. No. 0.0002;
Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY      1 RILAVERYLKDQQLGWCSGKLC 26
Db      589 RVTAEIKYLDQQLNSWGCAFRQVC 614

RESULT 63
VCLJG3
env polypeptide - simian immunodeficiency virus (macaque isolate)
C:Species: simian immunodeficiency virus, SIV
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 07-Nov-1997
C:Accession: H28887
R:Chakrabarti, L.; Guyader, M.; Alison, M.; Daniel, M.D.; Desrosiers, R.C.; Tiollais, P.
Nature 328, 543-547, 1987
A:Title: Sequence of simian immunodeficiency virus from macaque and its relationship to
A:Reference number: A28887; MUID:87287230; PMID:3649576
A:Accession: H28887
A:Molecule type: DNA
A:Residues: 1-881 <CHA>
A:Cross-references: GB:Y00277; GB:M16403; NID:G61730
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polypeptide
C:Keywords: AIDS; capsid protein; coat protein; immunodeficiency; polypeptide; transmembrane protein
Query Match      59.7%; Score 83; DB 1; Length 881;
Best Local Similarity 50.0%; Pred. No. 0.0002;
```

```
Db      568 RVTAEIKYLDQQLNSWGCAFRQVC 593

RESULT 59
VCLJGG
env polypeptide precursor - human immunodeficiency virus type 2 (isolate GH-1)
N;Alternate names: coat polypeptide
C:Species: human immunodeficiency virus type 2, HIV-2
A:Note: Host Homo sapiens (man)
C:Date: 30-Jun-1990 #sequence_revision 26-Jan-1996 #text_change 16-Feb-1997
C:Accession: JS0334
R:Hasegawa, A.; Tsujimoto, H.; Maki, N.; Ishikawa, K.; Miura, T.; Fukasawa, M.; Miki, K.
AIDS Res. Hum. Retroviruses 5, 593-604, 1989
A:Title: Sequence of a distinct HIV-2 isolate from Ghana showing significant divergence
A:Reference number: JS0327; MUID:90122350; PMID:2611042
A:Accession: JS0334
A:Molecule type: DNA
A:Residues: 1-852 <HAS>
A:Note: this sequence was submitted to JIPID, October 1989
A:Note: readthrough of the UAG stop codon at 739 may occur
C:Comment: Cleavage sites that yield the mature coat proteins are not determined.
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polypeptide
C:Keywords: AIDS; coat protein; glycoprotein; polypeptide; transmembrane protein
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-852/Product: env polypeptide #status predicted <MAT>
F;36,69,113,117,118,132,141,169,182,197,229,232,263,269,280,291,301,356,362,389,402,439,
Query Match      59.7%; Score 83; DB 1; Length 852;
Best Local Similarity 50.0%; Pred. No. 0.00019;
Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY      1 RILAVERYLKDQQLGWCSGKLC 26
Db      569 RVTAEIKYLDQQLNSWGCAFRQVC 594

RESULT 60
VCLJCT
env polypeptide precursor - human immunodeficiency virus type 2 (isolate CAM2/Guinea-Bissau)
N;Alternate names: coat polypeptide
C:Species: human immunodeficiency virus type 2, HIV-2
A:Note: Host Homo sapiens (man)
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jun-2000
C:Accession: F38475; J00978
R:Tristem, M.; Hill, F.; Karpas, A.
J. Gen. Virol. 72, 721-724, 1991
A:Title: Nucleotide sequence of a Guinea-Bissau-derived human immunodeficiency virus type 2
A:Reference number: A38475; MUID:91170959; PMID:2005437
A:Accession: F38475
A:Molecule type: DNA
A:Residues: 1-859 <TRI>
A:Cross-references: GB:D00835; NID:G3153166; PIDN:BARA00716.1; PID:G221472
C:Comment: The cleavage sites of this polypeptide have not been determined.
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polypeptide
C:Keywords: AIDS; coat protein; glycoprotein; immunodeficiency; polypeptide; transmembrane protein
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-859/Product: env polypeptide #status predicted <ENP>
F;38,71,115,148,163,176,188,195,205,237,247,271,277,288,299,309,343,366,398,411,448,463;
Query Match      59.7%; Score 83; DB 1; Length 859;
Best Local Similarity 50.0%; Pred. No. 0.0002;
Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY      1 RILAVERYLKDQQLGWCSGKLC 26
Db      579 RVTAEIKYLDQQLNSWGCAFRQVC 604

RESULT 61
S24571
env protein - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
C:Accession: S24571
R:Dietrich, U.
submitted to the EMBL Data Library, August 1989
A:Reference number: S24571
A:Accession: S24571
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-859 <DIE>
A:Cross-references: EMBL:X61240; NID:G60256; PIDN:CAA43572.1; PID:G60257
C:Superfamily: type E retrovirus env polypeptide
Query Match      59.7%; Score 83; DB 2; Length 859;
Best Local Similarity 50.0%; Pred. No. 0.0002;
Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY      1 RILAVERYLKDQQLGWCSGKLC 26
Db      580 RVTAEIKYLDQQLNSWGCAFRQVC 605

RESULT 62
S53098
envelope polypeptide - human immunodeficiency virus type 2
C:Species: human immunodeficiency virus type 2, HIV-2
C:Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 26-Aug-1999
C:Accession: S53098
R:Becker, M.; Zorr, B.; Becker, A.; Habermehl, K.O.
submitted to the EMBL Data Library, March 1995
A:Description: Molecular and phylogenetic characterisation of a Guinea-Bissau-derived human immunodeficiency virus type 2
A:Reference number: S53091
A:Accession: S53098
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-869 <BEC>
A:Cross-references: EMBL:Z48731; NID:G732718; PIDN:CAA88627.1; PID:G732736
C:Superfamily: type E retrovirus env polypeptide
C:Keywords: polypeptide
Query Match      59.7%; Score 83; DB 2; Length 869;
Best Local Similarity 50.0%; Pred. No. 0.0002;
Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY      1 RILAVERYLKDQQLGWCSGKLC 26
Db      589 RVTAEIKYLDQQLNSWGCAFRQVC 614

RESULT 63
VCLJG3
env polypeptide - simian immunodeficiency virus (macaque isolate)
C:Species: simian immunodeficiency virus, SIV
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 07-Nov-1997
C:Accession: H28887
R:Chakrabarti, L.; Guyader, M.; Alison, M.; Daniel, M.D.; Desrosiers, R.C.; Tiollais, P.
Nature 328, 543-547, 1987
A:Title: Sequence of simian immunodeficiency virus from macaque and its relationship to
A:Reference number: A28887; MUID:87287230; PMID:3649576
A:Accession: H28887
A:Molecule type: DNA
A:Residues: 1-881 <CHA>
A:Cross-references: GB:Y00277; GB:M16403; NID:G61730
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polypeptide
C:Keywords: AIDS; capsid protein; coat protein; immunodeficiency; polypeptide; transmembrane protein
Query Match      59.7%; Score 83; DB 1; Length 881;
Best Local Similarity 50.0%; Pred. No. 0.0002;
```

Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

OY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
| : | : | : | : | : | : | : | : |
DB 595 RVSAIEKYLDQAQLNMGCAFRQVC 620

RESULT 64
S04322
env polyprotein - simian immunodeficiency virus (mangabey isolate F236)
N:Contains: 120K glycoprotein; 40K glycoprotein
C:Species: simian immunodeficiency virus SIV
A>Note: host Cercopithecus torquatus atys (sooty mangabey)
C>Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 26-Aug-1999
C:Accession: S04322
R:Hirsch, V.M.; Olmssted, R.A.; Murphey-Corb, M.; Purcell, R.H.; Johnson, P.R.
Nature 339, 389-392, 1989
A:Title: An African primate lentivirus (STV(sm)) closely related to HIV-2.
A:Reference number: S04237; MUID:89262053; PMID:2786147
A:Accession: S04322
A>Status: nucleic acid sequence not shown
A:Molecule type: genomic RNA
A:Residues: 1-885 <HIR>
A:Cross-references: EMBL:X14307; NID:g61741; PIDN:CAA32487.1; PID:g61746
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: Glycoprotein; polyprotein

Query Match 59.7%; Score 83; DB 2; Length 885;
Best Local Similarity 50.0%; Pred. No. 0.0002;
Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

OY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
| : | : | : | : | : | : | : | : |
DB 598 RVTAIEKYLDQAQLNSWGCAFRQVC 623

RESULT 65
T11555
env protein - simian immunodeficiency virus SIVsm
C:Species: simian immunodeficiency virus SIVsm
A:Variety: strain 62
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C:Accession: T11555
R:Hirsch, V.M.; Martin, J.E.; Dapolito, G.; Elkins, W.R.; London, W.T.; Goldstein, S.; J
J. Virol. 68, 2649-2661, 1994
A:Title: Spontaneous substitutions in the vicinity of the V3 analog affect cell tropism
A:Reference number: Z17284; MUID:94187106; PMID:8139042
A:Accession: T11555
A>Status: preliminary; translated from GB/EMBL/DDBB
A:Molecule type: DNA
A:Residues: 1-886 <HIR>
A:Cross-references: EMBL:U04985; NID:g451609; PIDN:AAA18063.1; PID:g451611
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein

Query Match 59.7%; Score 83; DB 2; Length 886;
Best Local Similarity 50.0%; Pred. No. 0.0002;
Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

OY 1 RILAVERYLKDQQLGIWGCSGKLIC 26
| : | : | : | : | : | : | : | : |
DB 599 RVTAIEKYLDQAQLNSWGCAFRQVC 624

RESULT 66
T11566
envelope glycoprotein - simian immunodeficiency virus SIVsm (strain E543)
C:Species: simian immunodeficiency virus SIVsm
A:Variety: strain E543
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text change 21-Jul-2000

A:Accession: C26262
A:Molecule type: DNA
A:Residues: 1-858 <GUY>
A:Cross-references: GB:M15390; NID:g1332361; PIDN:AAB00770.1; PID:g325749
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polypeptide
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprotein
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-858/Product: env polypeptide #status predicted <MAT>
F:18-501/Product: exterior membrane glycoprotein #status predicted <EXT>
F:502-858/Product: transmembrane glycoprotein #status predicted <TMM>
F:34,67,76,119,120,151,166,179,192,193,196,206,238,241,248,272,278,289,300,367,371,400,4

Query Match 56.8%; Score 79; DB 1; Length 858;
Best Local Similarity 46.2%; Pred. NO. 0.0008; 7; Mismatches 0; Gaps 0;
Matches 12; Conservative

QY 1 RILAVERYLKDQQLGWCGSKGLIC 26
Db 578 RVTAIEKYLQDQARLNSWGCAFEQC 603

Search completed: May 3, 2004, 06:22:48
Job time : 39 secs